

Result No.	Score	Query %			DB	ID	Description
		Match	Length				
1	532	34.5	292	2	A60547	hypothetical prote	
2	489.5	28.5	328	2	A45774	odorant receptor 2	
3	464.5	27.0	313	2	E45774	odorant receptor 8	
4	446	26.0	313	2	B23701	olfactory receptor	
5	445	25.9	312	2	I23701	olfactory receptor	
6	434	25.3	310	2	E23701	olfactory receptor	
7	433	25.2	311	2	JCS200	chemoreceptor TB33	
8	422	24.6	309	1	S51356	olfactory receptor	
9	419	24.4	321	2	H45774	odorant receptor 3	
10	416	24.2	314	2	S29707	olfactory receptor	
11	414.5	24.1	311	2	S23701	olfactory receptor	
12	414	24.1	312	2	S29708	olfactory receptor	
13	410	23.9	315	2	JC4658	olfactory receptor	
14	406	23.6	314	2	H23701	olfactory receptor	
15	404.5	23.5	320	2	S20573	olfactory receptor	
16	404	23.5	304	2	S29709	olfactory receptor	
17	403	23.5	314	2	A37286	olfactory receptor	
18	400.5	23.3	315	2	JCS5836	olfactory receptor	
19	395.5	23.0	313	2	S20571	olfactory receptor	
20	395.5	23.0	317	2	F45774	odorant receptor 4	
21	395.5	23.0	327	2	F23701	olfactory receptor	
22	394.5	23.0	314	2	S20572	olfactory receptor	
23	394	22.9	312	2	A46247	olfactory receptor	
24	390.5	22.7	312	2	A46750	olfactory receptor	
25	390	22.7	312	2	I23701	olfactory receptor	
26	390	22.7	344	2	I45774	odorant receptor 1	
27	388	22.6	319	2	JCS624	olfactory receptor	
28	385	22.4	316	2	A57069	olfactory receptor	
29	378	22.0	305	2	S29711	olfactory factor 0	

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-328 <NGA>

A;Experimental source: olfactory epithelium

A;Note: sequence extracted from NCBI backbone (NCBIP:127746)

C;Superfamily: olfactory receptor OR14

C;Keywords: olfaction; transmembrane protein

Query Match 28.5%; Score 489.5; DB 2; Length 328;

Best Local Similarity 34.6%; Pred. No. 6e-36;

Matches 102; Conservative 60; Mismatches 132; Indels 1; Gaps 1;

QY 22 FLLGIRGL-EQFHLWLSIPVCGLTATVGNITILVVVATEPVLHKPVFLCMLSTID 80

DB 12 FVILGPGLPNNYGLVSVVMPFVVCYTLIGNCTFTFLREKSLQKPMYIIMLAASD 71

QY 81 LAASVSTVPKLLAIFWCAGHISASACLAHMEFFIHAFCMWESTVILLAMAFDRYVAICHPL 140

DB 72 VLFSYTTLPKIIARWFGDGSISFVGCFTQMGFVHYEATVNALVALVMAFDRYVAVCNPL 131

QY 141 RVATILDTTIIAHGVAAVRGSLLMLPCPPFFIGRLNFCQSHVILHTYCEHMAVVKLAGG 200

DB 132 RYWNIVKESITLGLCVSWLLAEPTVLTIVIRATSLPYCASNTVIQCYCDHVSVTKLACI 191

QY 201 DTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVILRLSSHEARSKALGTGCGSHVCVILI 260

DB 192 DTRPYAFPALVSALVWLLTPLAFILFSYGSIVTVFTSSTGRUKLTSLTSCSQQIILTL 251

QY 261 SYTPALFSFTFRFGHHVPVHIHILLANVYLLPPALNPVYGVKTKQIRKRVVR 315

DB 252 FFLPCLNVLSSSLGHINADIQILVIMLYSLPMPINVIYCLRTKEAKELCR 306

RESULT 3

E45774

odorant receptor 8 - channel catfish

C;Species: Ictalurus punctatus (channel catfish)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C;Accession: E45774

R;Ngai, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.

Cell 72, 657-666, 1993

A;Title: The family of genes encoding odorant receptors in the channel catfish.

A;Reference number: A45774; MUID:93201590; PMID:7916654

A;Accession: E45774

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-313 <NGA>

A;Experimental source: olfactory epithelium

A;Note: sequence extracted from NCBI backbone (NCBIP:127748)

C;Superfamily: olfactory receptor OR14

C;Keywords: olfaction; transmembrane protein

Query Match

Best Local Similarity 27.0%; Score 464.5; DB 2; Length 313;

Matches 101; Conservative 65; Mismatches 127; Indels 9; Gaps 4;

QY 20 SVFFLLGIGLQFHLWLSIPVCGLTATVGNITILVVVATEPVLHKPVFLCMLSTI 79

DB 11 TTTFLTGFHDLGSEWGPILSIPYLLMFLSTSLTLIYLIISQRLHSPCMLILGLMAV 70

QY 80 DLAAVSSTVPKLLAIF---WCGAGHISASACLAHMEFFIHAFCMWESTVILLAMAFDRYVAI 136

DB 71 DLSPMIFCVPNMLLSLFPNWKG---ISLVCLVQMECIHCAGTFQSTILLWALDRFFAI 127

QY 137 CHPLRYATILDTTIIAHGVAAVRGSLLMLPCPPFFIGRLNFCQSHVILHTYCEHMAVVK 196

DB 128 CRPLYQKYMGMENFLKFIIFPVIRNLFFITTVSWAGKLTFTCETNEIDHCVEHMAVQ 187

QY 197 LAGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVILRLSSHEARSKALGTGCGSHVC 256

DB 188 LACGDISINNALGULLTVFLTITADFTITISYIVILVSILR--SGKACLKAVNCTITHII 245

QY 257 VILISYTPALFSFTFRFGHHVPVHIHILLANVYLLPPALNPVYGVKTKQIRKRVVR 316

DB 246 VMTVSLTFLALIAFLSYRIRNFSP--SSRVFLSTMYLFIQSCFNPIIYGVRTKEIRQFLKL 304

QY 317 FQ 318

DB 305 MK 306

RESULT 4

B23701

olfactory receptor F5 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 04-Sep-1998

C;Accession: B23701

R;Buck, L.; Axel, R.

Cell 65, 175-187, 1991

A;Title: A novel multigene family may encode odorant receptors: a molecular basis for

A;Reference number: A23701; MUID:91191556; PMID:1840504

A;Accession: B23701

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-313 <BUC>

A;Cross-references: GB:M64377

C;Superfamily: olfactory receptor OR14

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 26.0%; Score 446; DB 2; Length 313;

Best Local Similarity 33.3%; Pred. No. 4.2e-32;

Matches 107; Conservative 63; Mismatches 135; Indels 16; Gaps 4;

QY 9 MESPHTDVPSPVFFLLGIPGLEQFHLMLSLPVCGLGTATVGNITILVVVATEPVLHKP 68

DB 1 MSSTNQSSV--TEFLLGLSRQPQQQLLFLFLIMYLATVLGNLLIILAIGTDSRLHTP 58

QY 69 VYFLCMLSTIDLAASVSTVPKLLAIFWCAGHISASACLAHMEFFIHAFCMWESTVILLAM 128

DB 59 MYFFLSNLFSVDVCFPSSTTPKVLNHLILGSAISFSGCLTQLYFLAVFGNMDNFLAYM 118

QY 129 AFRVVAICHPYATILDTTIIAHGVAAVRGSLLMLPCPPFFIGRLNFCQSHVILHTY 188

DB 119 SYDRFVAICHPYHTYTKTRQCLVLLVGVSWVANMNCLLHILLMARKSFCADNMIPHF 178

QY 189 CEHMAVVKIACGDTPRNRYVGLTAALLVIGVDLFCIGLSYALIAQAVILRLSSHEARSKAL 248

DB 179 CDGTPLLLSCSDTHLNMELMILTEGAVVMVTFVFCILSIYIHTCAVLAVSSPRGGWKS 238

QY 249 GTCGSHVCVILISYTPALFSFP-----THRFQHHVPVHIHILLANVYLLPPALNPVYGV 304

DB 239 STCGSHLAVVCLFYGTIVAVYFNPSSSHLAGRDMAA-----AVMYAVVTMLNPFIYSL 292

QY 305 KTKQ---IRKRVVRVFGSGQ 321

DB 293 RNSDMKAALRKVKVLAAMRFPKQ 313

RESULT 5

I23701

olfactory receptor I14 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999

C;Accession: I23701

R;Buck, L.; Axel, R.

Cell 65, 175-187, 1991

A;Title: A novel multigene family may encode odorant receptors: a molecular basis for

A;Reference number: A23701; MUID:91191556; PMID:1840504

A;Accession: I23701

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-312 <BUC>

A;Cross-references: GB:M64391; NID:G205843; PIDN:AAA41754.1; PID:G205844

C;Superfamily: olfactory receptor OR14

C;Keywords: G protein-coupled receptor; transmembrane protein

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Query Match      25.9%; Score 445; DB 2; Length 312;
Best local Similarity 34.6%; Pred. No. 5.1e-32;
Matches 102; Conservative 58; Mismatches 133; Indels 2; Gaps 2;

Qy 22 FLLGLPGLEQFHLWLSLPVCGCLGTATVGNITILVVVATEPVLHKPVYFLFCLWLSITDL 81
Db 12 FLLGLPIPSVHLLFFALFLAWYLTILGNLLIILVRLDSDLHMPMYFLFSLNLSFSDL 71

Qy 82 AASVSTVPKLLAI FWCAGAGHTSASACLAHMPFFIHFACWMESTVLLAMAFDRYVAICHPLR 141
Db 72 CFSVSTVPKLLQNNQSQPSISYTGCLTQLYFFVFMGDMESFLIVVMAYDRYVAICPFLR 131

Qy 142 YATITDTITIAHIGVAAVVRGSLMLPCPFIFGRNLFCQSHVILHTYCEHMAVVKACGD 201
Db 132 YTTIMSTKFCASIVLLWMLTMTHTALLHTLLIARLSFCERNVILHFFCDISALKLSCSD 191

Qy 202 TRPNRVGLTRAAILVIGVDLFCIGLSYALIAQAVRLRSGSHEARSKALGTGCSHVCVILIS 261
Db 192 IYVNELMIYILGGIIITPIPELLIVMSVRIFFSILKFFSIQDIYKVPSTCGSHLSVVTLF 251

Qy 262 YTPALFSGFFTHRFQGHVPHVHIHLLANVYLLPPALNPVVVGKTKOIRKRVVRV 316
Db 252 Y-GTIFGIYLCPSGNNSTVK-EIAMAMMYTVVTPLNFFIYSLENRDMKRALIRV 304

RESULT 6
E23701
olfactory receptor I3 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C:Accession: E23701
R:Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A:Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A:Reference number: A23701; MUID:91191556; PMID:1840504
A:Accession: E23701
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-310 <BUC>
A:Cross-references: GB:M64385; NID:g205831; PID:AAA41748.1; PID:g205832
C:Superfamily: olfactory receptor OR14
C:Keywords: G protein-coupled receptor; transmembrane protein

```

Query Match	25.3%;	Score 434;	DB 2;	Length 310;
Best Local Similarity	33.8%;	Pred. No. 4.8e-31;		
Matches 101;	Conservative	66;	Mismatches 126;	Indels 4;
Gaps	4;			

RESULT 7
JC5200
chemoreceptor TB334 - rat
C:Species: Rattus norvegicus (Norway rat)
C:date: 27-Feb-1997 #sequence revision 27-Feb-1997 #text change 26-Aug-1999

C:Accession: J05200; PC4302
R:Thomas, M.B.; Haines, S.L.; Akeson, R.A.
Gene 178, 1-5, 1996
A:Title: Chemoreceptors expressed in taste, olfactory and male reproductive tissues.
A:Reference number: J05200; MUID:97080538; PMID:8921883
A:Accession: J05200
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-311 <THO1>
A:Cross-references: GB:U50947; NID:g1256388; PID:g1256389
A:Accession: PC4302
A>Status: preliminary
A:Molecule type: protein
A:Residues: 146-153;265-272 <THO2>
A:Experimental source: taste bud
C:Comment: This protein is coupled to a GTP-binding protein-mediated signal transduction
C:Genetics:
A:Gene: tb334
C:Superfamily: olfactory receptor OR14
C:Keywords: olfaction; taste bud; transmembrane protein
F:24-47/Domain: transmembrane #status predicted <TM1>
F:56-77/Domain: transmembrane #status predicted <TM2>
F:99-118/Domain: transmembrane #status predicted <TM3>
F:138-162/Domain: transmembrane #status predicted <TM4>
F:195-217/Domain: transmembrane #status predicted <TM5>
F:236-258/Domain: transmembrane #status predicted <TM6>
F:271-291/Domain: transmembrane #status predicted <TM7>

Query Match	25.2%;	Score	433;	DB	2;	Length	311;	
Best Local Similarity	34.9%;	Pred.	NO. 5.9e-31;					
Matches	107;	Conservative	52;	Mismatches	126;	Indels	22;	
							Gaps	7;
Qy	20	SVEFLGLTGPGL-EQFHLWLSPVCGTGTATVGNITILVVVATEPVLHKPVYFLCMLST	78					
Db	8	SEFFLRGISGPPEQQOQLLYGLFLC-MYLVLTGTVNLIILAIGSDPHLHTPMYFFLANISF	66					
Qy	79	IDLAASVSTVPKLLAIFWCGAGHISASACLAHMFHIFACMSESTVLLAMAFDRYVAICH	138					
Db	67	ADMGLISSTVTKMLFNVTQCHTISVTGCLTQMYLPMFMFGDLDSFFLANWYDRYVAICH	126					
Qy	139	PLRVATILDTITIAHGVAAVVRGSLMLPCPFPGICRLNFCQSHVILHTYCEHMAVVKLA	198					
Db	127	PHYSTIMNARICVLMILICWLTNTNVALTHTLLMARLSFCVVGEIAHFFCDVTSVMKLS	186					
Qy	199	CGDTRPNRV---YGLTRALLVIGVDLFCIGLSYALIAQAVLRLSHEARSKALGTCGSH	254					
Db	187	CSDTHVNLVLSGPGGT---VLMVPFVSIVSYVHIVFAVLRIQSSGGSGKAFSTCGSH	242					
Qy	255	VCVILISYTPALFSFFTHRFHGHVPHIHIH-----ILLANVYLLPPALNPVYGKTKQI	309					
Db	243	LCVVCVVFY-GTFLFSYVL-----FFSSVETTEKDVAAMAMYTVVTPMLNPFYISLRNKDI	295					
Qy	310	RKRVRV	316					
Db	296	KGALKRL	302					

RESULT 8
S51356
olfactory receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S51356; S47014
R.; Gat, U.; Nekrasova, E.; Lancet, D.; Natochin, M.
Eur. J. Biochem. 225, 1157-1168, 1994
A;Title: Olfactory receptor proteins. Expression, characterization and partial purification
A;Reference number: S51356; MUID:95045546; PMID:7957207
A;Accession: S51356
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-309 <GAT>
A;Cross-references: EMBL:X80671; NID:G517365; PIDN:CAA56697.1; PID:G517366
R.; Gat, U.; Nekrasova, E.; Lancet, D.; Natochin, M.

C;Accession: C23701
R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A;Reference number: A23701; MUID:91191556; PMID:1840504
A;Accession: C23701
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-311 <BUC>
A;Cross-references: GB:M64378; NID:g205817; PIDN:AAA41741.1; PID:g205818
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 24.1%; Score 414.5; DB 2; Length 311;
Best Local Similarity 31.4%; Pred. No. 2.6e-29;
Matches 103; Conservative 59; Mismatches 131; Indels 35; Gaps 8;

QY 1 MSSTLGHNMESPHHTDVPVSFVLGIPGLEQFHLWLSLFCVGLGTATVGNITILVVVA 60
DB 1 MAWSTGQNLST-----PGPILLGFGPGRSMRIGLELLFLVWVLLTVGNLALISLVG 53
QY 61 TEPVLHKPVYFLCMLSTIDLAASVSTVKPLAIFWCAGHISASACLAHMFPIHAFCMW 120
DB 54 AHRCLQTPMYPFLCNLSFLEIWFACVPTLATPAPRGVVISLACCATQMYFVSIGCT 113
QY 121 ESTVLLAMAFDRYVAICHPLRYATILDTIIAHIGVAAVVRG-SLLMLPCPFIFGLNFC 179
DB 114 EYFLAVMAYDRYLAICPLRYGGIMTPGLAMRLALGSLWLCGSAITVPAT-LIARLSFC 172
QY 180 QSHVILHYTCHEMAVAVKACGTRNVRVGLTAALLVI----GVDLFCIGLSYALIAQAV 235
DB 173 GSRVINHFCDISPWVLSCTDTQVVELVSFGIAFCVILGSGITL-----VSAYAIITI 228
QY 236 LRLSSHEARSKALGTCGSHVVCVILSYTPALPSFTHRFGHHVPVHH-----ILLA 287
DB 229 IKIPSGARGHRAFSCTSSHLTVLLIYWGSTIEL-----HVRTSVESLDTKAITVL 280
QY 288 NVYLLLPALNPVYGVKTKQIRKVRV 315
DB 281 NT--IVTPVLPNPFYITLRNKDVKEALRR 306

RESULT 12

S29708
olfactory receptor OR12 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
C;Accession: S29708
R;Raming, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.; Breer
Nature 361, 353-356, 1993
A;Title: Cloning and expression of odorant receptors.
A;Reference number: S29707; MUID:93149273; PMID:7678922
A;Accession: S29708
A;Molecule type: mRNA
A;Residues: 1-312 <RAM>
C;Superfamily: olfactory receptor OR14

Query Match 24.1%; Score 414; DB 2; Length 312;
Best Local Similarity 32.1%; Pred. No. 2.9e-29;
Matches 99; Conservative 64; Mismatches 121; Indels 24; Gaps 4;

QY 20 SVFFILGIP-GLGQHLWLSLPCVGLGTATVGNITILVVVATEPVILHKPVYFLCMLST 78
DB 10 SQFLLLGLFIPERHWHLFYTL-LLAMYLTLILGNLIILILLDSNLHITPMYFLNSLF 68
QY 79 IDLAASVSTVPKLLAIFWCAGHISASACLAHMFPIHAFCMWSTVLLAMAFDRYVAICH 138
DB 69 SLCFSSVTMPKLLQNMQNQDTSITYTGCLTQMYFSWVFGMEIFLLVSMAYDRYVAICL 128
QY 139 PLRYATILDTTIIAHIGVAAVVRGSLMLPCPFIFGLNFCQSHVILHYTCHEMAVVKLA 198
DB 129 PLHYTSIMSPKFCVCLGSLSWFNVLYSMLHTLLARLSFCKDNVPIPHFFCDISALLKLA 188

QY 199 CGDTRPNRNVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKALGTCGSHVCVI 258
DB 189 CSDTYINELMFIPLGGLLIVIPFELLIVMTYVQIVCSILKVPSTRAIYKIFSTCGSHLSTV 248
QY 259 LISYTPALPSFTHRFGHHVPVHI-----HILLANVYLLLPALNPVYGVKTKQ 308
DB 249 SLFY-----GTVIGLYLCPSSANNSTVKETVMAMMTVVVTPMLNPIYSLRND 296
QY 309 IRKRVVRV 316
DB 297 IKEALVRV 304

RESULT 13

JC4658
olfactory receptor - human
C;Species: Homo sapiens (man)
C;Date: 18-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
C;Accession: JC4658
R;Crowe, M.L.; Perry, B.N.; Connerton, I.F.
Gene 169, 247-249, 1996
A;Title: Olfactory receptor-encoding genes and pseudogenes are expressed in humans.
A;Reference number: JC4658; MUID:96194811; PMID:8647456
A;Accession: JC4658
A;Molecule type: DNA
A;Residues: 1-315 <CRO>
A;Cross-references: EMBL:X80391; NID:g516319; PIDN:CAA56602.1; PID:g516320
A;Experimental source: olfactory epithelial cells
C;Comment: This receptor belongs to a family of ligand-binding proteins involved in sign.

A;Gene: Twbt

A;Map position: 17
C;Superfamily: olfactory receptor OR14
C;Keywords: receptor; signal transduction; transmembrane protein
F;29-54/Domain: transmembrane #status predicted <TM1>
F;60-81/Domain: transmembrane #status predicted <TM2>
F;101-123/Domain: transmembrane #status predicted <TM3>
F;142-160/Domain: transmembrane #status predicted <TM4>
F;199-220/Domain: transmembrane #status predicted <TM5>
F;239-262/Domain: transmembrane #status predicted <TM6>
F;275-295/Domain: transmembrane #status predicted <TM7>

Query Match 23.9%; Score 410; DB 2; Length 315;
Best Local Similarity 32.3%; Pred. No. 6.6e-29;
Matches 97; Conservative 56; Mismatches 135; Indels 12; Gaps 4;

QY 22 FFLGLI---PGLEQ---FHLWLSLPCVGLGTATVGNITILVVVATEPVILHKPVYFLCML 76
DB 15 FILLGLLEAPGLQPVVFLFLFAYL-----VTVRGNLSLAAVLEPKLHTPMYFLGNL 69
QY 77 STIDLAASVSTVPKLLAIFWCAGHISASACLAHMFPIHAFCMWSTVLLAMAFDRYVAI 136
DB 70 SVLDVGCISVTVPSMLSRLSRKRAVPCGACLTQLFFHLFVGVDFCLLTAMAYDQFLAI 129
QY 137 CHPLRYATILDTTIIAHIGVAAVVRGSLMLPCPFIFGLNFCQSHVILHYTCHEMAVVK 196
DB 130 CRPLTYSTRMSQTVORMLVAAWACAFNTALHTVTAMSTLNPFCGNNVINHFCDLPQLEQ 189
QY 197 LACGTRPNRNVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKALGTCGSHVC 256
DB 190 LSCSSTQLNEILLFPAVGFTMAGTPMALIVISYIHVAAVLRISVEGRKKAFTSCGSHLT 249
QY 257 VLLISYTPALPSFTHRFGHHVPVHHILLANVYLLLPALNPVYGVKTKQIRKVRV 316
DB 250 VVAIFYSGIENYM--RLGSTKLSKDKKAVGIFNTVINPMLNPIIYSFRNPVDVQAIWRM 307

RESULT 14

H23701
olfactory receptor I9 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C;Accession: H23701

Db	121	TNCFLLTAMGYDRYVAICNPLFYMWIMNKRRLIQVLWGACSIGLIVAITQVTSVFRLPFC	180
Qy	180	QSHVILHTYCEHMAVVKACGDTNRNVYGLTAALLVIGVDLFCIGLSVALLAQAVLRLS	239
Db	181	-ARKVPHEFCDIRPMKLSCIDTTVNEILTISVLVLVPMGLVFISVLLIISTILKTA	239
Qy	240	SHEARSKALGTGCGSHVCVILISYTPALSFFFTHREGHVHPVHHIHLANVLLPPALNP	299
Db	240	SVEGRKKAFATCASHLTVMVHYSCASTAYLKPK-SENTREHDQ-LISVTYTVITFELNP	297
Ov	300	VYGVYKTKOIRKVVVR	315

```
Db      298 VVYTLRKEVKDLCR 313
          ||| :| :||| :
Search completed: September 15, 2004, 21:37:53
Job time : 19 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 21:35:29 ; Search time 18 Seconds
(without alignments)
943.608 Million cell updates/sec

Title: US-10-081-775-2

Perfect score: 1718

Sequence: 1 MSSTLGHNMSPHHTDVPDPS.....RKRVRVVFQSGQGMKASE 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	861	50.1	320	4	US-09-439-313-527
2	861	50.1	320	4	US-09-636-215-527
3	861	50.1	320	4	US-09-685-166A-527
4	856	49.8	320	1	US-08-465-980-2
5	856	49.8	320	2	US-09-053-303-2
6	856	49.8	320	4	US-09-339-115-2
7	856	49.8	320	5	PCT-US95-07093-2
8	429	25.0	321	3	US-08-748-506-18
9	428.5	24.9	321	3	US-08-748-506-20
10	424	24.7	321	3	US-08-748-506-10
11	423.5	24.7	321	3	US-08-748-506-12
12	416.5	24.2	321	3	US-08-748-506-11
13	413	24.0	284	1	US-08-118-270-61
14	413	24.0	284	5	PCT-US93-08528-61
15	412.5	24.0	321	3	US-08-748-506-19
16	410.5	23.9	321	3	US-08-748-506-13
17	410	23.9	321	3	US-09-546-986A-6
18	410	23.9	340	4	US-09-524-730-6
19	401	23.3	310	4	US-09-546-986A-2
20	401	23.3	310	4	US-09-524-730-2
21	394.5	23.0	314	3	US-08-988-876-7
22	393	22.9	296	2	US-08-467-948A-2
23	393	22.9	296	3	US-08-467-947A-2
24	388.5	22.6	309	3	US-08-988-876-5
25	381	22.2	334	4	US-09-546-986A-8
26	381	22.2	334	4	US-09-524-730-8
27	374	21.8	316	2	US-08-827-291A-2

28 367 21.4 333 3 US-08-988-876-6 Sequence 6, Appli
29 361 21.0 247 1 US-08-465-980-3 Sequence 3, Appli
30 361 21.0 247 2 US-09-053-303-3 Sequence 3, Appli
31 361 21.0 247 4 US-09-339-115-3 Sequence 3, Appli
32 361 21.0 247 5 PCT-US95-07093-3 Sequence 3, Appli
33 349.5 20.3 284 1 US-08-118-270-67 Sequence 67, Appli
34 349.5 20.3 284 5 PCT-US93-08528-67 Sequence 67, Appli
35 341.5 19.9 327 3 US-08-748-506-22 Sequence 22, Appli
36 341.5 19.9 327 3 US-08-748-506-23 Sequence 23, Appli
37 341 19.8 222 2 US-08-467-948A-27 Sequence 27, Appli
38 341 19.8 222 3 US-08-467-947A-27 Sequence 27, Appli
39 340 19.8 277 1 US-08-118-270-62 Sequence 62, Appli
40 340 19.8 277 5 PCT-US93-08528-62 Sequence 62, Appli
41 333.5 19.4 286 1 US-08-118-270-65 Sequence 65, Appli
42 333.5 19.4 286 5 PCT-US93-08528-65 Sequence 65, Appli
43 332 19.3 327 3 US-08-748-506-24 Sequence 24, Appli
44 330 19.2 277 1 US-08-118-270-68 Sequence 68, Appli
45 330 19.2 277 5 PCT-US93-08528-68 Sequence 68, Appli

ALIGNMENTS

RESULT 1

US-09-439-313-527

; Sequence 527, Application US/09439313

; Patent No. 6329505

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan Louise

; APPLICANT: Jiang Yuqul

; APPLICANT: Reed, Steven G.

; APPLICANT: Kalos, Michael

; APPLICANT: Fanger, Gary

; APPLICANT: Retter, Mark

; APPLICANT: Soik, John

; APPLICANT: Day, Craig

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

; FILE REFERENCE: 210121.427C9

; CURRENT APPLICATION NUMBER: US/09/439,313

; CURRENT FILING DATE: 1999-11-12

; NUMBER OF SEQ ID NOS: 575

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 527

; LENGTH: 320

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-439-313-527

Query Match 50.1%; Score 861; DB 4; Length 320;

Best Local Similarity 53.8%; Pred. No. 8e+74;

Matches 161; Conservative 49; Mismatches 89; Indels 0; Gaps 0;

QY 20 SVFLLGIPGLEQHMLSLPVGGLGTATIVGNITLVVATEPVLHPKPVYFLCMLSTI 79

Db 9 ATFVLIGIPGLEKAHFVVGFPFLLSMYYVVMFGNCIVFIVRTSLHAPMVLFLCMLAAI 68

QY 80 DLAAVSVPKLLAIFWCGAGHISASACLAHMFTHAFCMMESTVILLAMAFDRYVAICHP 139

Db 69 DLALSTTMPKLLALFWPDSREISFEACLTQFMFFIHALSAIESITILLAMAFDRYVAICHP 128

QY 140 LRYATILTDITIAHIGVAAVVRGSLMLPCPFGRNLNFCQSHVILHTYCEHMAVVKLAC 199

Db 129 LRHAALNNTVTAIGIVAVVRGSLFFPFLPLLKRLAFCHSNVLSHSYCVHQDVMKLAY 188

QY 200 GDTFPRNVYGLTAALLVIGVDLFCIGISYALIAQAVLRLSHSHEARSKALGTCGSHVCVIL 259

Db 189 ADTLPNVYVYGLTALLVGVDMVFISLYFLIIRTVLQLPSKSERAKAFGTCVSHGVVL 248

QY 260 ISYTPALFSPFTHRFPGHVPVHIILLANVLLPPALNPVYVYGVYKTKQIKRVRVRFQ 318


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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,980
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 320 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-465-980-2

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Query Match      49.8%; Score 856; DB 1; Length 320;
Best Local Similarity 54.2%; Pred. No. 2.4e-73;
Matches 160; Conservative 48; Mismatches 87; Indels 0; Gaps 0;

QY 24 LLGIPGLEQFHLWLSLPCVCLGTATVGNITILVVVATEPVVHKPVYFLCMLSTIDLAA 83
Db 13 LLGIPGLEKAFHWGFPVLLSMVVMVAMCNCIVFIVRTSRSHAPMYFLCMLAAIDLAL 72
QY 84 SVSTVPKLLAIFWCAGAGHISASACLAHMFHFAFCMESTVLLAMAFDHYVAICHPLRYA 143
Db 73 STSTMPKLLALFWPDSREISIEACLTQMTFFIHLSAESTILLAMAFDHYVAICHPLRHA 132
QY 144 TILDTTIIAHGVAAVVRGSLMLPCPFIFGRNFCQSHVILHTYCEHMAVVKLAGDTR 203
Db 133 AVLNTVTVAQIGVAVVRGSLFFFLPLLLIKRLAFCHSNVLSHSCVHQDVMKLAYADTL 192
QY 204 PNRVYGLTAALLVIGVDLFCIGLSYALTAQAQVLRLLSSHEARSKALGTCGSHVCVILISYT 263
Db 193 PNVYGLTALLVMGVDVNFISLSTYFLIRTVLQPLPSKERAKAFGTCVSHIGVVLAFVY 252
QY 264 PALFSFTHRHGHVPHVHIHILLANVYLLPALNPVYGVKTKQIRKRVVRVQ 318
Db 253 PLIGLSVVRHFGNSLHPVRVVMGDIYLLLPVNPVPIYGAKTKQIRTRVLAMFK 307

```

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RESULT 5
US-09-053-303-2
; Sequence 2, Application US/09053303
; Patent No. 5948890
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Li, Yi
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPAJ70
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,303
; FILING DATE:

```

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,980
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 320 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-053-303-2

Query Match      49.8%; Score 856; DB 2; Length 320;
Best Local Similarity 54.2%; Pred. No. 2.4e-73;
Matches 160; Conservative 48; Mismatches 87; Indels 0; Gaps 0;

QY 24 LLGIPGLEQFHLWLSLPCVCLGTATVGNITILVVVATEPVVHKPVYFLCMLSTIDLAA 83
Db 13 LLGIPGLEKAFHWGFPVLLSMVVMVAMCNCIVFIVRTSRSHAPMYFLCMLAAIDLAL 72
QY 84 SVSTVPKLLAIFWCAGAGHISASACLAHMFHFAFCMESTVLLAMAFDHYVAICHPLRYA 143
Db 73 STSTMPKLLALFWPDSREISIEACLTQMTFFIHLSAESTILLAMAFDHYVAICHPLRHA 132
QY 144 TILDTTIIAHGVAAVVRGSLMLPCPFIFGRNFCQSHVILHTYCEHMAVVKLAGDTR 203
Db 133 AVLNTVTVAQIGVAVVRGSLFFFLPLLLIKRLAFCHSNVLSHSCVHQDVMKLAYADTL 192
QY 204 PNRVYGLTAALLVIGVDLFCIGLSYALTAQAQVLRLLSSHEARSKALGTCGSHVCVILISYT 263
Db 193 PNVYGLTALLVMGVDVNFISLSTYFLIRTVLQPLPSKERAKAFGTCVSHIGVVLAFVY 252
QY 264 PALFSFTHRHGHVPHVHIHILLANVYLLPALNPVYGVKTKQIRKRVVRVQ 318
Db 253 PLIGLSVVRHFGNSLHPVRVVMGDIYLLLPVNPVPIYGAKTKQIRTRVLAMFK 307

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RESULT 6
US-09-339-115-2
; Sequence 2, Application US/09339115
; Patent No. 6372891
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Li, Yi
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPAJ70
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/339,115
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

```

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; APPLICATION NUMBER: 09/053,303
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 320 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-07093-2

Query Match          49.8%; Score 856; DB 4; Length 320;
Best Local Similarity 54.2%; Pred. No. 2,4e-73;
Matches 160; Conservative 48; Mismatches 87; Indels 0; Gaps 0;

QY 24 LIGIPLEGFHLWLSLPCVGLGTATIVGNITLVVVAPEVLHKPVYFLCMLSTIDLAA 83
Db 13 LIGIPLEGKHPVGFPLLSMYVWAMCGNCIVFIVRTSLHAPMYFLCMLAAIDLAL 72
QY 84 SVSTVPKLLAIWCGAGHISASACLAHMFHAFCMWESTVLLAMAFDRYVAICHPLRYA 143
Db 73 STTMPKILALFWFDSREISIEACLTQMFHIALSAIESITILLAMAFDRYVAICHPLREA 132
QY 144 TILDTITIAHIGVAAVVRGSLMLPCPPFIFGRINFCQSHVILHTYCEHMAVVKLACGDT 203
Db 133 AVLNNTVTAQIGIVAVRGSLEFFFLPLIKLAFCHSNVLSHCYCHQDVWKLAYADTL 192
QY 204 PNRVGLTAALIVIGVDLFCIGLSYALIAQAVLRSLSSHEARSKALGTCSGSHVCVILISYT 263
Db 193 PNVVGLTALLVMGVDMFISLSYFLIIRTVLQLPSKERAKAFGTCVSHIGVLAFFV 252
QY 264 PALFSEFFTHRGHHVPVHIILLANVYLLPALNPVVYGVTKQIRKRVVRVQ 318
Db 253 PLIGLSVVRHFGNSLHPVVRVWVGDIYLLPPVINPIYGAKTKQIRTRVLAMFK 307

RESULT 7
PCT-US95-07093-2
; Sequence 2, Application PC/TUS9507093
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Li, Yi
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAU70
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07093
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,980
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 320 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-07093-2

Query Match          49.8%; Score 856; DB 5; Length 320;
Best Local Similarity 54.2%; Pred. No. 2,4e-73;
Matches 160; Conservative 48; Mismatches 87; Indels 0; Gaps 0;

QY 24 LIGIPLEGFHLWLSLPCVGLGTATIVGNITLVVVAPEVLHKPVYFLCMLSTIDLAA 83
Db 13 LIGIPLEGKHPVGFPLLSMYVWAMCGNCIVFIVRTSLHAPMYFLCMLAAIDLAL 72
QY 84 SVSTVPKLLAIWCGAGHISASACLAHMFHAFCMWESTVLLAMAFDRYVAICHPLRYA 143
Db 73 STTMPKILALFWFDSREISIEACLTQMFHIALSAIESITILLAMAFDRYVAICHPLREA 132
QY 144 TILDTITIAHIGVAAVVRGSLMLPCPPFIFGRINFCQSHVILHTYCEHMAVVKLACGDT 203
Db 133 AVLNNTVTAQIGIVAVRGSLEFFFLPLIKLAFCHSNVLSHCYCHQDVWKLAYADTL 192
QY 204 PNRVGLTAALIVIGVDLFCIGLSYALIAQAVLRSLSSHEARSKALGTCSGSHVCVILISYT 263
Db 193 PNVVGLTALLVMGVDMFISLSYFLIIRTVLQLPSKERAKAFGTCVSHIGVLAFFV 252
QY 264 PALFSEFFTHRGHHVPVHIILLANVYLLPALNPVVYGVTKQIRKRVVRVQ 318
Db 253 PLIGLSVVRHFGNSLHPVVRVWVGDIYLLPPVINPIYGAKTKQIRTRVLAMFK 307

RESULT 8
US-08-748-506-18
; Sequence 18, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voigt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 18:

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Query Match	24.9%;	Score 428.5;	DB 3;	Length 321;
Best Local Similarity	35.3%;	Pred. No. 7.6e-33;		
Matches 106;	Conservative 51;	Mismatches 132;	Indels 11;	Gaps 4;

QY	27	IPGLEQFHLWLSLPCVGLGTATVGNITILVVVATEPVHLKPVYFLCMLSTIDLAASVS	86
Db	26	VPG-ECFLFTLIILMFL--VSTGNTLIILALAICTSPSLHTPMYFFFLANLSLLEIGVTC	82
QY	87	TVPKLLAIFWCAGGHISASACLAHMFPIHAFCMWSTVLLAMAFDRYVAICHPLRYATIL	146
Db	83	VIPKWLQSLVSEARGISWEGCASQMFPIFGTECCLLAAMAFDRYMAICSPHLVATRM	142
QY	147	TDTIAIHGAUVVGRSLLMLPCPFFIGRILNFCQSHVILHTYCEHMAVWVKLACGDRPNR	206
Db	143	SRGVCAYLAIVSWVMGCIIVGLQTNFIISLFCGPCEIDHFFCDLPPLLALACGDTSQNE	202
QY	207	VYGLTAALLVIGDVLFCIGLSYALIAQAVLRSLSHEARSALGTCSGHVCVIILISTPAL	266
Db	203	AAIFVAVAVLCIFSPFLIIISYVRILVAVLWMPSEGRHKALSTCSHLLVWTLFYGSTS	262
QY	267	FSFTHFRGHVPVPHIILLANVLLPPLNPNVYGVKTKQJLRKRVVRVFGSQQGMGIK	326
Db	263	ATYLRSSKSHSPGV--DKLLALFVTSVMSLNFIIYSLRNKEVKGLRRT-----LGLK	314

RESULT 10

US-08-748-506-10

; Sequence 10, Application US/08748506

; Patent No. 6159707

; GENERAL INFORMATION:

; APPLICANT: Ronnett et al.

; TITLE OF INVENTION: NOVEL SPERM RECEPTORS

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Leydig, Voit & Mayer, Ltd.

; STREET: Two Prudential Plaza, Suite 4900

; CITY: Chicago

; STATE: IL

; COUNTRY: US

; ZIP: 60601-6780

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/748,506

; FILING DATE: 08-NOV-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/033,751

; FILING DATE: 09-NOV-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; REFERENCE/DOCKET NUMBER: 74940

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-616-5600

; TELEFAX: 312-616-5700

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 321 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-748-506-10

Query Match	24.7%;	Score 424;	DB 3;	Length 321;
Best Local Similarity	34.4%;	Pred. No. 2e-32;		
Matches 96;	Conservative 48;	Mismatches 127;	Indels 8;	Gaps 2;

QY	48	TIVGNITILVVVATEPVHLKPVYFLCMLSTIDLAASVTPVKLLAIFWCAGGHISASAC	107
Db	47	IVGNTILVVVATEPVHLKPVYFLCMLSTIDLAASVTPVKLLAIFWCAGGHISASAC	107

Db	44	SLTGNLVLIACTSPSLHTPMYFFLANLSLEIGYTCVSPKPMQLSVSEAREISREGC	103
QY	108	LAHMEFFIHAFCMESTVLLAMAFDRYVAICHPLRYATILDTIIAHIGVAAVVRGSLML	167
Db	104	ATQMEFFAFFGITECCLLAAMAFDRMAICSPLHYATRMSREVCAHLAIVSWGMCIVSL	163
QY	168	PCPFFIGRLNFCQSHVILHTYCEHMAVVKACGDRPNRVYGLTAALLVIGVDLFCIGLS	227
Db	164	GOTNEIFSLNFCGCEIDHFFCDLPPLLALACGDTSONEAAIFVVAVLICISSPFLLIYS	223
QY	228	YALIAQAVLRSLSSHEARSKALGTCSGSHVCVILISYTPALFSFTHRGHVPVHIHILIA	287
Db	224	YKILIAVLLMSPGRHKALGTCSHLLVVLVFGSACITVLRPKSSH--SPGMDKFLA	281
QY	288	NYLLLPALNPVVYGVKTKQIRKRVVRVFGSQGGMGIK	326
Db	282	LFYTVTSMNLNPIIYSLRNKEVKALRRT-----LGLK	314
RESULT 11			
US-08-748-506-12			
; Sequence 12, Application US/08748506			
; Patent No. 6159707			
; GENERAL INFORMATION:			
; APPLICANT: Romnett et al.			
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS			
; NUMBER OF SEQUENCES: 31			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.			
; STREET: Two Prudential Plaza, Suite 4900			
; CITY: Chicago			
; STATE: IL			
; COUNTRY: US			
; ZIP: 60601-6780			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/748,506			
; FILING DATE: 08-NOV-1996			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 60/033,751			
; FILING DATE: 09-NOV-1995			
; CLASSIFICATION: 435			
; ATTORNEY/AGENT INFORMATION:			
; REFERENCE/DOCKET NUMBER: 74940			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 312-616-5600			
; TELEFAX: 312-616-5700			
; INFORMATION FOR SEQ ID NO: 12:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 321 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-748-506-12			
Query Match 24.7%; Score 423.5; DB 3; Length 321;			
Best Local Similarity 35.0%; Pred. No. 2.3e-32;			
Matches 105; Conservative 51; Mismatches 133; Indels 11; Gaps 4;			
QY	27	IPGLEQFHLWLSLPVCGLTGATIVGNITILVVATEPVLHKPVYLFCLMLSTIDLAASVS	86
Db	26	VPG-ECFLFTLILMLF--VSLTGNLIALAICTSPSLHTPMYFFLANLSLEIGYTC	82
QY	87	TVPKLLAIFWCGAGHISASACLAHMFHAFCMWESTVLLAMAFDRYVAICHPLRYATIL	146
Db	83	VIPKMLQSLVSEARGISWEGCASQMFPIFGITECCLLAAMAFDRYMAICSPPLHYATRM	142
QY	147	TDITIAHIGVAAVVRGSLMLPCPFFIGRLNFCQSHVILHTYCEHMAVVKACGDRPNR	206
Db	143	ATYLRKSKSHSPGV--DKLLALFYTSVTSMNLNPIIYSLRNKEVKALRRT-----LGLK	314
RESULT 12			
US-08-748-506-11			
; Sequence 11, Application US/08748506			
; Patent No. 6159707			
; GENERAL INFORMATION:			
; APPLICANT: Romnett et al.			
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS			
; NUMBER OF SEQUENCES: 31			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.			
; STREET: Two Prudential Plaza, Suite 4900			
; CITY: Chicago			
; STATE: IL			
; COUNTRY: US			
; ZIP: 60601-6780			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/748,506			
; FILING DATE: 08-NOV-1996			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 60/033,751			
; FILING DATE: 09-NOV-1995			
; CLASSIFICATION: 435			
; ATTORNEY/AGENT INFORMATION:			
; REFERENCE/DOCKET NUMBER: 74940			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 312-616-5600			
; TELEFAX: 312-616-5700			
; INFORMATION FOR SEQ ID NO: 11:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 321 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-748-506-11			
Query Match 24.2%; Score 416.5; DB 3; Length 321;			
Best Local Similarity 34.1%; Pred. No. 1e-31;			
Matches 102; Conservative 48; Mismatches 144; Indels 5; Gaps 3;			
QY	27	IPGLEQFHLWLSLPVCGLTGATIVGNITILVVATEPVLHKPVYLFCLMLSTIDLAASVS	86
Db	26	VPG-ECFLFTLILMLF--VSLTGNLIALAICTSPSLHTPMYFFLANLSLEIGYTC	82
QY	87	TVPKLLAIFWCGAGHISASACLAHMFHAFCMWESTVLLAMAFDRYVAICHPLRYATIL	146
Db	83	VIPKMLQSLVSEAREISRECATQMFFTFGITECCLLAAMAFDRCMGICSPPLHYATRM	142
QY	147	TDITIAHIGVAAVVRGSLMLPCPFFIGRLNFCQSHVILHTYCEHMAVVKACGDRPNR	206
Db	143	SREVCALHAIVSWGMCIVGLGQTNIXSLNFCGCPCEIDHFFCDLPPLLALACGDTSONE	202
QY	207	VYGLTAALLVIGVDLFCIGLSYALIAQAVLRSLSSHEARSKALGTCSGSHVCVILISYTPAL	266
Db	203	AAIFVAAAILCISSPFLIYSYVRILVAVLVMPSPFGRHKALSTCSSHLLVVLVTFYGSVS	262

QY 267 FGFTHFRGHVPHVHIHLLANVYLLPPALNPVYGVKTKQIRKRVVRVFGSQGMGI 325
Db 263 FYLRPKSH--SPGMDKLLALFYTAVTSMNLNFIYSLRNKEVKAALRRRLDLJKIMSI 319

RESULT 13
US-08-118-270-61
; Sequence 61, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 284 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-118-270-61

Query Match 24.0%; Score 413; DB 1; Length 284;
Best Local Similarity 33.6%; Pred. No. 1.9e-31;
Matches 95; Conservative 56; Mismatches 114; Indels 18; Gaps 5;

QY 47 ATIVGNITILVVVATEPVHLKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASA 106
Db 12 ATVLGNLLIILAIGDSRLHTPMYFNLSDVDFVCSSTVPKLVANHLGSQLISFG 71

QY 107 CLAHMFFHAFCMESTVLLAMADRYVAICHPLRYATILDTIIAHIGVAAVVRGSLIM 166
Db 72 CLTQLYFLAVFGNMDNFLAVMSYDHYVAICHPLHYTTIRQLCVLLVVGSWVANNCIL 131

QY 167 LPCPFFIGRLNFCQSHVILHTYCEHMAVVKLACGDTRENVVGLTAALLVIGVDLFCIGL 226
Db 132 --HILIMARKSCAD--LPHFCDGTPLKLSGSDTHNELMILTEGAVVWVTPVCIL 187

QY 227 SYALIAQAVLRSLSSHEARSKALGTCGSHVCVILISYTPALFSFF----THRFGHHVPVHI 282
Db 198 SYIHTCAVLRVSSPRGKWSFSTCGSHIAVVCFLYGTIVAVYFNPSPSSHLAGRDMAA-- 245

QY 283 HILLANVYLLPPALNPVYGVKTKQ----IRKRVVRVFGSQ 321
Db 284

Db 246 ----AVMYAVVTPMINPFIYSLRNSDMKAALRKVLAMRFPFSKQ 284

RESULT 14
PCT-US93-08528-61
; Sequence 61, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 284 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-08528-61

Query Match 24.0%; Score 413; DB 5; Length 284;
Best Local Similarity 33.6%; Pred. No. 1.9e-31;
Matches 95; Conservative 56; Mismatches 114; Indels 18; Gaps 5;

QY 47 ATIVGNITILVVVATEPVHLKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASA 106
Db 12 ATVLGNLLIILAIGDSRLHTPMYFNLSDVDFVCSSTVPKLVANHLGSQLISFG 71

QY 107 CLAHMFFHAFCMESTVLLAMADRYVAICHPLRYATILDTIIAHIGVAAVVRGSLIM 166
Db 72 CLTQLYFLAVFGNMDNFLAVMSYDHYVAICHPLHYTTIRQLCVLLVVGSWVANNCIL 131

QY 167 LPCPFFIGRLNFCQSHVILHTYCEHMAVVKLACGDTRENVVGLTAALLVIGVDLFCIGL 226
Db 132 --HILIMARKSCAD--LPHFCDGTPLKLSGSDTHNELMILTEGAVVWVTPVCIL 187

QY 227 SYALIAQAVLRSLSSHEARSKALGTCGSHVCVILISYTPALFSFF----THRFGHHVPVHI 282
Db 188 SYIHTCAVLRVSSPRGKWSFSTCGSHIAVVCFLYGTIVAVYFNPSPSSHLAGRDMAA-- 245

QY 283 HILLANVYLLPPALNPVYGVKTKQ----IRKRVVRVFGSQ 321
Db 246 ----AVMYAVVTPMINPFIYSLRNSDMKAALRKVLAMRFPFSKQ 284

RESULT 15
US-08-748-506-19

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; Sequence 19, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnett et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-748-506-19

Query Match      24.0%; Score 412.5; DB 3; Length 321;
Best Local Similarity 34.1%; Pred. No. 2.5e-31;
Matches 102; Conservative 48; Mismatches 144; Indels 5; Gaps 3;

QY 27 IPCLEQFHLWLSIPVCGLTGATIVGNITILVVVATEPVVHKPVYFLCLMLSTIDLAASVS 86
Db 26 VPG-ECFLFTLILMFL--VSLTGALIALAACTSPSLHTPMYFFLANLSLLEIGYCS 82
QY 87 TVPKLIAIFWCGAGHISASACLAHMFPIHAFCMWESTVLIAMAFDRYVAICHPLRYATIL 146
Db 83 VIPKMLQSLVSEAREISREGCATQMFFFTFFGITECCLLAAMAFDRCMGICSPHYATRM 142
QY 147 TDTIIAHGVAAVRGSLLMLPCPFPIGRINFCQSHVILHTYCEHMAVVKLACGDRPNR 206
Db 143 SREVCALAIVSWGMCIVGLGQTNIIISLNFQCPCEIDHFFCDLPPLALACGDTSQNE 202
QY 207 VYGLTAALVIGVDLFCIGLSYALIAQAVILSLSSHEARSKALGTCGSHVCVILISYTPAL 266
Db 203 AALFVAALICISPPFVILYSYVRILVAVLVMPSPGRKALSTCSSHLVLTFLFYGSVS 262
QY 267 FSFTHRFHGHVPHVHIILANVYLLPPALNPVYGVKTKQIRKRVVRVFGSQGMGI 325
Db 263 FTVLRPKSSH--SPGMDKLLALFYTAVTSMNLNPIIYSLRNKEVKAALRRRLDLKKIMSI 319
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Search completed: September 15, 2004, 21:38:17
Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 21:36:29 ; Search time 50 Seconds
(without alignments)
2110.138 Million cell updates/sec

Title: US-10-081-775-2

Perfect score: 1718

Sequence: 1 MSSTLGHNMESPHHTDVPDPS.....RKRVRVFGQGMGIKASE 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1718	100.0	329	14	US-10-081-775-2
2	1691	98.4	329	9	US-09-886-055-261
3	1691	98.4	329	10	US-09-804-291-261
4	1691	98.4	329	12	US-10-343-650A-354
5	1691	98.4	329	14	US-10-025-806-36
6	1691	98.4	329	14	US-10-025-806-38
7	1691	98.4	329	15	US-10-292-798-798
8	1649	96.0	321	15	US-10-017-161-924
9	1649	96.0	321	16	US-10-017-161-924
10	936.5	54.5	299	15	US-10-292-798-834
11	931.5	54.2	329	12	US-10-343-650A-316
12	931.5	54.2	329	15	US-10-387-629-158
13	931.5	54.2	329	15	US-10-292-798-820
14	931.5	54.2	329	15	US-10-467-252-45
15	931.5	54.2	329	16	US-10-467-252-45

16	920	53.6	326	12	US-10-182-822A-2	Sequence 2, Appli
17	907	52.8	311	14	US-10-044-643-20	Sequence 20, Appl
18	904	52.6	311	9	US-09-886-055-113	Sequence 113, App
19	904	52.6	311	10	US-09-804-291-113	Sequence 113, App
20	904	52.6	311	12	US-10-343-650A-214	Sequence 214, App
21	904	52.6	311	14	US-10-220-382-10	Sequence 10, Appl
22	904	52.6	311	14	US-10-044-643-16	Sequence 16, Appl
23	904	52.6	311	15	US-10-292-798-784	Sequence 784, App
24	903	52.6	311	14	US-10-044-643-18	Sequence 18, Appl
25	901.5	52.5	329	14	US-10-025-806-26	Sequence 26, Appl
26	889.5	51.8	314	14	US-10-017-161-878	Sequence 878, App
27	889.5	51.8	318	9	US-09-886-055-101	Sequence 101, App
28	889.5	51.8	318	10	US-09-804-291-101	Sequence 101, App
29	889.5	51.8	318	11	US-09-981-566A-56	Sequence 56, Appl
30	889.5	51.8	318	11	US-09-981-566A-101	Sequence 101, App
31	889.5	51.8	318	12	US-10-343-650A-198	Sequence 198, App
32	889.5	51.8	318	14	US-10-081-775-5	Sequence 5, Appli
33	889.5	51.8	318	14	US-10-044-643-55	Sequence 55, Appl
34	889.5	51.8	318	15	US-10-005-041A-38	Sequence 38, Appl
35	889.5	51.8	322	14	US-10-025-806-2	Sequence 4, Appli
36	888.5	51.7	322	14	US-10-025-806-4	Sequence 4, Appli
37	887.5	51.7	326	10	US-09-966-459A-14	Sequence 14, Appl
38	887.5	51.7	326	11	US-09-981-566A-54	Sequence 54, Appl
39	887.5	51.7	326	11	US-09-981-566A-99	Sequence 99, Appl
40	887.5	51.7	326	14	US-10-219-834-76	Sequence 76, Appl
41	887.5	51.7	326	14	US-10-044-643-57	Sequence 57, Appl
42	887.5	51.7	326	15	US-10-005-041A-36	Sequence 36, Appl
43	887.5	51.7	326	15	US-10-005-041A-60	Sequence 60, Appl
44	887.5	51.7	326	16	US-10-323-412-14	Sequence 14, Appl
45	886.5	51.6	321	16	US-10-466-720-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-10-081-775-2

; Sequence 2, Application US/10081775

; Publication No. US20030060409A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED

; TITLE OF INVENTION: RECEPTOR, HGPRTM25, EXPRESSED HIGHLY IN IMMUNE-RELATED TISSUES

; FILE REFERENCE: D0126 NP

; CURRENT APPLICATION NUMBER: US/10/081,775

; CURRENT FILING DATE: 2002-02-21

; PRIOR APPLICATION NUMBER: US 60/270,134

; PRIOR FILING DATE: 2001-02-21

; PRIOR APPLICATION NUMBER: US 60/278,952

; PRIOR FILING DATE: 2001-03-27

; NUMBER OF SEQ ID NOS: 69

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 2

; LENGTH: 329

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-081-775-2

Query Match 100.0%; Score 1718; DB 14; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.5e-155;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSSTLGHNMESPHHTDVPDPSVFFLLGIPGLWLSLPVCGLTATVGNITILVVVA	60
Db	1	MSSTLGHNMESPHHTDVPDPSVFFLLGIPGLWLSLPVCGLTATVGNITILVVVA	60
QY	61	TEPVLRKPYVFLCMLSTIDIAASVTPVKLLAIFWCAGHISASACLAHFFHAFQCM	120
Db	61	TEPVLRKPYVFLCMLSTIDIAASVTPVKLLAIFWCAGHISASACLAHFFHAFQCM	120
QY	121	ESTVLLAMAFDRYVAICHPLRYATILDTTIAHIGVAAVRGSLLMLPCPFIFGLNFQO	180
Db	121	ESTVLLAMAFDRYVAICHPLRYATILDTTIAHIGVAAVRGSLLMLPCPFIFGLNFQO	180


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/ SEQ ID NO 354
/ LENGTH: 329
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-343-650A-354

Query Match
Best Local Similarity 98.4%; Score 1691; DB 12; Length 329;
Matches 325; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSTLGHNMESPHHTDVSFVFLGLPGLEQPHLWLSLVPVCGLTATVGNITILVVVA 60
Db 1 MSTLGHNMESPHHTDVSFVFLGLPGLEQPHLWLSLVPVCGLTATVGNITILVVVA 60
QY 61 TEPVLHKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMEFIHAFNM 120
Db 61 TEPVLHKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMEFIHAFNM 120
QY 121 ESTVLLAMAFDRYVAICHPLRYATILTDITIIAHIGVAAVVRGSLMLPCPPFFIGRLNFCQ 180
Db 121 ESTVLLAMAFDRYVAICHPLRYATILTDITIIAHIGVAAVVRGSLMLPCPPFFIGRLNFCQ 180
QY 181 SHVILHTYCEHMAVVKACGDRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRSS 240
Db 181 SHVILHTYCEHMAVVKACGDRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRSS 240
QY 241 HEARSKALGTCGSHVCVILISYTPALFSFTHRFHGHVPHVHIHLLANVYLLPPALNPV 300
Db 241 HEARSKALGTCGSHVCVILISYTPALFSFTHRFHGHVPHVHIHLLANVYLLPPALNPV 300
QY 301 VYGVTQKQIRKRVVRVFGSQGGMGIKASE 329
Db 301 VYGVTQKQIRKRVVRVFGSQGGMGIKASE 329

RESULT 5
US-10-025-806-36
/ Sequence 36, Application US/10025806
/ Publication No. US20030198955A1
/ GENERAL INFORMATION:
/ APPLICANT: Li, Li
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Ballinger, Robert
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Colman, Steven
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Casman, Stacie
/ APPLICANT: Edinger, Shlomit
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Sciore, Paul
/ APPLICANT: Smithson, Glennnda
/ APPLICANT: Peyman, John
/ APPLICANT: MacDougall, John
/ APPLICANT: Stone, David
/ APPLICANT: Vernet, Corine
/ APPLICANT: Shenoy, Suresh
/ APPLICANT: Gunther, Erik
/ APPLICANT: Millet, Isabelle
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Anderson, David
/ APPLICANT: Gusev, Vladimir
/ APPLICANT: Malyankar, Uriel
/ APPLICANT: Zhong, Haihong
/ APPLICANT: Ellerman, Karen
/ APPLICANT: Wolenc, Adam
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-224 AB
/ CURRENT APPLICATION NUMBER: US/10/025, 806
/ CURRENT FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 60/256, 635
/ PRIOR FILING DATE: 2000-12-18
/ PRIOR APPLICATION NUMBER: 60/259, 743
/ PRIOR FILING DATE: 2001-01-04
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/ PRIOR APPLICATION NUMBER: 60/299, 327
/ PRIOR FILING DATE: 2001-06-19
/ PRIOR APPLICATION NUMBER: 60/261, 498
/ PRIOR FILING DATE: 2001-01-12
/ PRIOR APPLICATION NUMBER: 60/263, 689
/ PRIOR FILING DATE: 2001-01-24
/ PRIOR APPLICATION NUMBER: 60/276, 464
/ PRIOR FILING DATE: 2001-02-08
/ PRIOR APPLICATION NUMBER: 60/271, 021
/ PRIOR FILING DATE: 2001-02-22
/ PRIOR APPLICATION NUMBER: 60/275, 946
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/278, 150
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: 60/285, 718
/ PRIOR FILING DATE: 2001-04-23
/ PRIOR APPLICATION NUMBER: 60/312, 902
/ PRIOR FILING DATE: 2001-08-16
/ PRIOR APPLICATION NUMBER: 60/257, 876
/ PRIOR FILING DATE: 2000-12-21
/ PRIOR APPLICATION NUMBER: 60/260, 718
/ PRIOR FILING DATE: 2001-01-10
/ PRIOR APPLICATION NUMBER: 60/284, 591
/ PRIOR FILING DATE: 2001-04-18
/ NUMBER OF SEQ ID NOS: 352
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 36
/ LENGTH: 329
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-025-806-36

Query Match
Best Local Similarity 98.4%; Score 1691; DB 14; Length 329;
Matches 325; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSTLGHNMESPHHTDVSFVFLGLPGLEQPHLWLSLVPVCGLTATVGNITILVVVA 60
Db 1 MSTLGHNMESPHHTDVSFVFLGLPGLEQPHLWLSLVPVCGLTATVGNITILVVVA 60
QY 61 TEPVLHKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMEFIHAFNM 120
Db 61 TEPVLHKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMEFIHAFNM 120
QY 121 ESTVLLAMAFDRYVAICHPLRYATILTDITIIAHIGVAAVVRGSLMLPCPPFFIGRLNFCQ 180
Db 121 ESTVLLAMAFDRYVAICHPLRYATILTDITIIAHIGVAAVVRGSLMLPCPPFFIGRLNFCQ 180
QY 181 SHVILHTYCEHMAVVKACGDRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRSS 240
Db 181 SHVILHTYCEHMAVVKACGDRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRSS 240
QY 241 HEARSKALGTCGSHVCVILISYTPALFSFTHRFHGHVPHVHIHLLANVYLLPPALNPV 300
Db 241 HEARSKALGTCGSHVCVILISYTPALFSFTHRFHGHVPHVHIHLLANVYLLPPALNPV 300
QY 301 VYGVTQKQIRKRVVRVFGSQGGMGIKASE 329
Db 301 VYGVTQKQIRKRVVRVFGSQGGMGIKASE 329
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RESULT 6
US-10-025-806-38
/ Sequence 38, Application US/10025806
/ Publication No. US20030198955A1
/ GENERAL INFORMATION:
/ APPLICANT: Li, Li
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Ballinger, Robert
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Colman, Steven
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Casman, Stacie
```



```
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 924
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-924

Query Match          96.0%; Score 1649; DB 14; Length 321;
Best Local Similarity 98.8%; Pred. No. 9.3e-149;
Matches 317; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 MESPHTDVPDSVFFLLGIPGLEQPHLWLSLPVCGLGATATVGNITILVVVATEPVLHKP 68
Db 1 MESPHTDVPDSVFFLLGIPGLEQPHLWLSLPVCGLGATATVGNITILVVVATEPVLHKP 60

QY 69 VYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHFFFIHAFCMESTVLLAM 128
Db 61 VYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHFFFIHAFCMESTVLLAM 120

QY 129 AFDRYVAICHPLRYATILTDTTIIAHIGVAAVVRGSLMLPCPFFIGRLNFCQSHVILHTY 188
Db 121 AFDRYVAICHPLRYATILTDTTIIAHIGVAAVVRGSLMLPCPFFIGRLNFCQSHVILHTY 180

QY 189 CEHMAVVKACGDTPRNRYGLTAALLVIGVDLFCIGLSYALIAQAVRLSSHEARSKAL 248
Db 181 CEHMAVVKACGDTPRNRYGLTAALLVIGVDLFCIGLSYALIAQAVRLSSHEARSKAL 240

QY 249 GTCGSHVCVILISYTPALFSFFTHRGHHVPVHIHILLANVYLLPPALNPVVYGVKTKQ 308
Db 241 GTCGSHVCVILISYTPALFSFFTHRGHHVPVHIHILLANVYLLPPALNPVVYGVKTKQ 300

QY 309 IRKRVVRVFSQGGMGKASE 329
Db 301 IRKRVVRVFSQGGMGKASE 321

RESULT 9
US-10-297-021-19
; Sequence 19, Application US/10297021
; Publication No. US20040023294A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: YAO, Monique G.
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: THORNTON, Michael
; APPLICANT: LU, Yan
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: AU-YOUNG, Janice
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: SF-0781 PCT
; CURRENT APPLICATION NUMBER: US/10/297,021
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 60/206,222; 60/207,476; 60/208,834; 60/208,861; 60/209,868
; PRIOR FILING DATE: 2000-05-22; 2000-05-25; 2000-06-02; 2000-06-02; 2000-06-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 321
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023294A1 7476077CD1
US-10-297-021-19

Query Match          96.0%; Score 1649; DB 16; Length 321;
Best Local Similarity 98.8%; Pred. No. 9.3e-149;
Matches 317; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 MESPHTDVPDSVFFLLGIPGLEQPHLWLSLPVCGLGATATVGNITILVVVATEPVLHKP 68
Db 1 MESPHTDVPDSVFFLLGIPGLEQPHLWLSLPVCGLGATATVGNITILVVVATEPVLHKP 60

QY 69 VYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHFFFIHAFCMESTVLLAM 128
Db 61 VYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHFFFIHAFCMESTVLLAM 120

QY 129 AFDRYVAICHPLRYATILTDTTIIAHIGVAAVVRGSLMLPCPFFIGRLNFCQSHVILHTY 188
Db 121 AFDRYVAICHPLRYATILTDTTIIAHIGVAAVVRGSLMLPCPFFIGRLNFCQSHVILHTY 180

QY 189 CEHMAVVKACGDTPRNRYGLTAALLVIGVDLFCIGLSYALIAQAVRLSSHEARSKAL 248
Db 181 CEHMAVVKACGDTPRNRYGLTAALLVIGVDLFCIGLSYALIAQAVRLSSHEARSKAL 240

QY 249 GTCGSHVCVILISYTPALFSFFTHRGHHVPVHIHILLANVYLLPPALNPVVYGVKTKQ 308
Db 241 GTCGSHVCVILISYTPALFSFFTHRGHHVPVHIHILLANVYLLPPALNPVVYGVKTKQ 300

QY 309 IRKRVVRVFSQGGMGKASE 329
Db 301 IRKRVVRVFSQGGMGKASE 321

RESULT 10
US-10-292-798-834
; Sequence 834, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 834
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-834

Query Match          54.5%; Score 936.5; DB 15; Length 299;
Best Local Similarity 58.4%; Pred. No. 7.2e-81;
Matches 173; Conservative 48; Mismatches 74; Indels 1; Gaps 1;

QY 25 LGIPGLEQPHLWLSLPVCGLGATATVGNITILVVVATEPVLHKPVLFLCMLSTIDLAAS 84
Db 1 MGIEPASHFWIAFPFCSTALAVLGNMNVLLVHSEPVHLHQPMYFLCMLSTIDLVLC 60

QY 85 VSTVPKLLAIFWCGAGHISASACLAHFFFIHAFCMESTVLLAMAFDRYVAICHPLRYAT 144
Db 61 TSTVPKLLALFWAKDAEINFACAAQMFHIGSAVESGILLANAFDRYVAICHPLHYGS 120

QY 145 ILDTTIIAHIGVAAVVRGSLMLPCPFFIGRLNFCQSHVILHTYCEHMAVVKACGTRP 204
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QY 259 LISYTPALFSFFTHRFHGHVPHVHIILLANVYLLPPALNPVYGVKTKQIRKRVRVF 317
Db 267 LVFYVPGIFSFLTHRFHGHVPHVHVLLATRYLLMPPALNPVYGVKTKQIRQRLRVF 325

RESULT 14
US-10-292-798-820
; Sequence 820, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 820
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-820

Query Match 54.2%; Score 931.5; DB 15; Length 329;
Best Local Similarity 59.9%; Pred. No. 2.4e-80;
Matches 179; Conservative 42; Mismatches 77; Indels 1; Gaps 1;

QY 19 PSVFFLLGIPGLEQPHLMVSLPVCGLGTATVGNITILVVVATEPVLPKPVYFLCMLST 78
Db 28 PS-FLLVGIPGLEESQHWIALPLGILYLLALVGNVTILFIWMDFSLHQSMLYFLSMLAA 86
QY 79 IDLAASVSTVPKLLAIFWCAGHISASACLAHMFHAFCMESTVLLAMAFDRYVAICH 138
Db 87 IDLVASSTAPKALAVLLVHAHEIGYIVLCIQMFFHAFSSMESGVLMALDRYVAICH 146
QY 139 PLRYATILTDITIAHIGVAAVVRGSLMLPCPFIFGRNLNFCOSHVILHTYCEHMAVVKLA 198
Db 147 PLHSTILHPGVIGRGMVLRGULLLIPFILLGTILFCQATIIIGHAYCEHMAVVKLA 206
QY 199 CGDTPNRYVGLTALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKALGTGCGSHVCVI 258
Db 207 CSETTVNRAYGLTMALLVIGLDVLAIGVSYAHILQAVLKVPVPGSEARLKAFSTCGSHICVI 266
QY 259 LISYTPALFSFFTHRFHGHVPHVHIILLANVYLLPPALNPVYGVKTKQIRKRVRVF 317
Db 267 LVFYVPGIFSFLTHRFHGHVPHVHVLLATRYLLMPPALNPVYGVKTKQIRQRLRVF 325

RESULT 15
US-10-467-252-45
; Sequence 45, Application US/10467252
; Publication No. US20040115676A1
; GENERAL INFORMATION:
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: NGUYEN, Daniel B.; THORNTON, Michael;
; APPLICANT: YAO, Monique G.; KALLICK, Deborah A.;
; APPLICANT: GANDHI, Ameena R.; CHAWLA, Narinder K.
; APPLICANT: ARVIZU, Chandra S.; ELLIOTT, Vicki S.;
; APPLICANT: HAFALIA, April J.A.; RAMKUMAR, Jayalaxmi;
; APPLICANT: JIN, Pei; TANG, Y. Tom;
; APPLICANT: YUE, Henry; REDDY, Roopa
; APPLICANT: BUREFORD, Neil; LU, Dyung Aina M.;
; APPLICANT: GAUL, Richard C.; KAHN, Farrah A.;
; APPLICANT: WALSH, Roderick T.; ISON, Craig H.;
; APPLICANT: RICHARDSON, Thomas W.; GRIFFIN, Jennifer A.
; APPLICANT: WARREN, Bridget A.; YANG, Junming;
```

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; APPLICANT: LEE, Ernestine A.; HARLAND, Lee
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0357 USN
; CURRENT APPLICATION NUMBER: US/10/467,252
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: PCT/US02/03635
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/267,322;
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: US 60/271,215
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/274,551
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/278,507
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/280,597
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/281,107
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/282,121
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PERL Program
; SEQ ID NO 45
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7475226CD1
US-10-467-252-45

Query Match 54.2%; Score 931.5; DB 16; Length 329;
Best Local Similarity 59.9%; Pred. No. 2.4e-80;
Matches 179; Conservative 42; Mismatches 77; Indels 1; Gaps 1;

QY 19 PSVFFLLGIPGLEQPHLMVSLPVCGLGTATVGNITILVVVATEPVLPKPVYFLCMLST 78
Db 28 PS-FLLVGIPGLEESQHWIALPLGILYLLALVGNVTILFIWMDFSLHQSMLYFLSMLAA 86
QY 79 IDLAASVSTVPKLLAIFWCAGHISASACLAHMFHAFCMESTVLLAMAFDRYVAICH 138
Db 87 IDLVASSTAPKALAVLLVHAHEIGYIVLCIQMFFHAFSSMESGVLMALDRYVAICH 146
QY 139 PLRYATILTDITIAHIGVAAVVRGSLMLPCPFIFGRNLNFCOSHVILHTYCEHMAVVKLA 198
Db 147 PLHSTILHPGVIGRGMVLRGULLLIPFILLGTILFCQATIIIGHAYCEHMAVVKLA 206
QY 199 CGDTPNRYVGLTALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKALGTGCGSHVCVI 258
Db 207 CSETTVNRAYGLTMALLVIGLDVLAIGVSYAHILQAVLKVPVPGSEARLKAFSTCGSHICVI 266
QY 259 LISYTPALFSFFTHRFHGHVPHVHIILLANVYLLPPALNPVYGVKTKQIRKRVRVF 317
Db 267 LVFYVPGIFSFLTHRFHGHVPHVHVLLATRYLLMPPALNPVYGVKTKQIRQRLRVF 325

Search completed: September 15, 2004, 21:39:13
Job time : 52 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 21:33:43 ; Search time 13 Seconds
(without alignments)
1317.775 Million cell updates/sec

Title: US-10-081-775-2
Perfect score: 1718
Sequence: 1 MGSTLGHNMESPHHTDVPDPS.....RKRVVRVFGQGMGIKASE 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1649	96.0	321	1 OYP1_HUMAN	Q8nh57 homo sapien
2	931.5	54.2	314	1 OYL1_HUMAN	Q8nh70 homo sapien
3	904	52.6	311	1 OYJ3_HUMAN	Q8nh60 homo sapien
4	889.5	51.8	318	1 OYD1_HUMAN	Q8h346 homo sapien
5	885.5	51.5	321	1 OYN4_HUMAN	Q8ngi2 homo sapien
6	883.5	51.4	304	1 OYL2_HUMAN	Q8nghe6 homo sapien
7	881.5	51.3	314	1 OYK1_HUMAN	Q8ngk4 homo sapien
8	873	50.8	324	1 OYN5_HUMAN	Q8nh56 homo sapien
9	871	50.7	320	1 OXE2_RAT	Q88628 rattus norv
10	867.5	50.5	325	1 OYE2_HUMAN	Q8ngj4 homo sapien
11	866.5	50.4	320	1 OYN1_HUMAN	Q8nh53 homo sapien
12	866	50.4	314	1 OYK2_HUMAN	Q8ngk3 homo sapien
13	861	50.1	320	1 OXE1_HUMAN	Q9h255 homo sapien
14	847.5	49.3	317	1 OXE2_HUMAN	Q8tc66 homo sapien
15	842	49.0	321	1 OYD2_HUMAN	Q8ngi0 homo sapien
16	838.5	48.8	312	1 OYE4_HUMAN	Q8ng99 homo sapien
17	838	48.8	315	1 OYR1_HUMAN	Q8ngf1 homo sapien
18	830.5	48.3	317	1 OYB2_HUMAN	Q8ngf0 homo sapien
19	822	47.8	314	1 OYB6_HUMAN	Q8ngd2 homo sapien
20	808	47.0	314	1 OXG2_HUMAN	Q8ngf0 homo sapien
21	801	46.6	314	1 OYH1_HUMAN	Q8ngk0 homo sapien
22	788.5	45.9	315	1 OYE5_HUMAN	Q8ngj2 homo sapien
23	788	45.9	321	1 OXG1_HUMAN	Q8nh55 homo sapien
24	788	45.9	330	1 OXF2_HUMAN	Q8ngk1 homo sapien
25	787	45.8	308	1 OYF1_HUMAN	Q8nh61 homo sapien
26	784	45.6	312	1 OYI2_HUMAN	Q8ngj3 homo sapien
27	782.5	45.5	313	1 OYE6_HUMAN	Q8h344 homo sapien
28	772	44.9	315	1 OXL1_HUMAN	Q8ngd3 homo sapien
29	761.5	44.3	312	1 OYAL_HUMAN	Q8ngj5 homo sapien
30	755	43.9	314	1 OYB4_HUMAN	Q8uk12 homo sapien
31	744.5	43.3	313	1 OXAA_HUMAN	Q8ngk2 homo sapien
32	730	42.5	314	1 OXII_HUMAN	Q8ngj6 homo sapien
33	725.5	42.2	313	1 OXAZ_HUMAN	Q8ngj7 homo sapien

34	703.5	40.9	312	1 OXA7_HUMAN	Q8nh64 homo sapien
35	702	40.9	317	1 OXQ1_HUMAN	Q8nh59 homo sapien
36	695.5	40.5	324	1 OYI2_HUMAN	Q8nh67 homo sapien
37	679.5	39.6	324	1 OYI1_HUMAN	Q8ngk6 homo sapien
38	677	39.4	302	1 OXH1_HUMAN	Q8nh63 homo sapien
39	673.5	39.2	315	1 OXM1_HUMAN	Q8h341 homo sapien
40	668	38.9	327	1 OXT1_HUMAN	Q8ngj9 homo sapien
41	622	36.2	312	1 OXB2_HUMAN	Q8y5p1 homo sapien
42	621.5	36.2	314	1 OZA1_HUMAN	Q8nght5 homo sapien
43	611.5	35.6	313	1 OZA4_HUMAN	Q8nght8 homo sapien
44	593.5	34.5	322	1 OZB2_HUMAN	Q8ngi1 homo sapien
45	576	33.5	323	1 OXS1_HUMAN	Q8ngj8 homo sapien

ALIGNMENTS

RESULT 1
OYPI_HUMAN STANDARD; PRT; 321 AA.
AC Q8NH57;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 52p1.
GN OR52P1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Putami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes".
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);
MW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&

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or send an email to license@isb-sib.ch).

EMBL; AB065534; BAC05780.1; ALT_INIT.
Genew; HGNC:15232; OR52P1.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOFSN.
DR PROSITE; PS00237; G-PROTEIN_RECF F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECF F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
Multigene family; Olfaction.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 48 1 (POTENTIAL).
FT DOMAIN 49 56 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 57 77 2 (POTENTIAL).
FT DOMAIN 78 101 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 102 122 3 (POTENTIAL).
FT DOMAIN 123 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 162 4 (POTENTIAL).
FT DOMAIN 163 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 219 5 (POTENTIAL).
FT DOMAIN 220 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 260 6 (POTENTIAL).
FT DOMAIN 261 275 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 276 296 7 (POTENTIAL).
FT DOMAIN 297 315 CYTOPLASMIC (POTENTIAL).
FT DISULFID 99 191 BY SIMILARITY.
FT CARBOHYD 5 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 321 AA; 34889 MW; 47329FE6ADC8CF22 CRC64;
Query Match 96.0%; Score 1649; DB 1; Length 321;
Best Local Similarity 98.8%; Pred. No. 4.7e-123;
Matches 317; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 9 MESPHTDVPDFVLLGPGLEQFHLMSLPVCGLGATIVGNITILVVVATEPVLPK 68
DB 1 MESPHTDVPDFVLLGPGLEQFHLMSLPVCGLGATIVGNITILVVVATEPVLPK 60
QY 69 VYLFCLMSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFHFAFCMMESTVLLAM 128
DB 61 VYLFCLMSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFHFAFCMMESTVLLAM 120
QY 129 AFDYVAICHPURYATILTDTIIAHIGVAAVVRGSLMLPCFFFGRLNFCQSHVILHTY 188
DB 121 AFDYVAICHPURYATILTDTIIAHIGVAAVVRGSLMLPCFFFGRLNFCQSHVILHTY 180
QY 189 CEHMAVVKLACGDTFRPNRYVGLTAALLVIGDLCFGLSYALIAQAVLRSLSSHEARSKAL 248
DB 181 CEHMAVVKLACGDTFRPNRYVGLTAALLVIGDLCFGLSYALIAQAVLRSLSSHEARSKAL 240
QY 249 GTCGSHVCVILSYTPALFSFTHRGHHVPVHHIHLANVLLPPALNPVYGVKTKQ 308
DB 241 GTCGSHVCVILSYTPALFSFTHRGHHVPVHHIHLANVLLPPALNPVYGVKTKQ 300
QY 309 IRKRVVRVPSQGGMGKASE 329
DB 301 IRKRVVRVPSQGGMGKASE 321

RESULT 2

OYJ3_HUMAN STANDARD; PRT; 314 AA.
AC Q8NH67;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 52J3.
GN OR52L1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Teutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
receptor genes";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB065819; BAC06038.1; ALT_INIT.
CC Genew; HGNC:14785; OR52L1.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 29 49 1 (POTENTIAL).
FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 58 78 2 (POTENTIAL).
FT DOMAIN 79 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 123 3 (POTENTIAL).
FT DOMAIN 124 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 163 4 (POTENTIAL).
FT DOMAIN 164 199 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 200 220 5 (POTENTIAL).
FT DOMAIN 221 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 261 6 (POTENTIAL).
FT DOMAIN 262 276 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 277 297 7 (POTENTIAL).
FT DOMAIN 298 314 CYTOPLASMIC (POTENTIAL).
FT DISULFID 100 192 BY SIMILARITY.
FT CARBOHYD 5 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 314 AA; 34557 MW; 6C022206DB6C1520 CRC64;
Query Match 54.2%; Score 931.5; DB 1; Length 314;
Best Local Similarity 59.9%; Pred. No. 1.6e-66;
Matches 179; Conservative 42; Mismatches 77; Indels 1; Gaps 1;
QY 19 PSVFFLLGPGLEQFHLMSLPVCGLGATIVGNITILVVVATEPVLPKPVFLCMLST 78
DB 13 PS-FLLVGPGLEESQHWALPLGILYLALVGNVTILFIWDPDLHQSMYLFSLMLAA 71
QY 79 IDLAASVSTVPKLLAIFWCGAGHISASACLAHMFHFAFCMMESTVLLAMAFDRVVAICH 138
DB 72 IDLVLASSTAPKALAVLLVHAHEIGYIVCLIQMFFIHAFSSGVLVAMALDRVVAICH 131
QY 139 PLRYATILTDTIIAHIGVAAVVRGSLMLPCFFFGRLNFCQSHVILHTYCEHMAVVKLA 198
DB 132 PLHSTILHPGVIGRGNVIVRGVLLLPFLPILLGLTFLCOATIIIGHAYCEHMAVVKLA 191
QY 199 CGDTRPNRYVGLTAALLVIGDLCFGLSYALIAQAVLRSLSSHEARSKALGTCGSHVCVI 258
DB 192 CSETTVNRAYGLTMALLVIGDLCFGLSYALIAQAVLRSLSSHEARSKALGTCGSHVCVI 251
QY 259 LISYTPALFSFTHRGHHVPVHHIHLANVLLPPALNPVYGVKTKQIRKRVVRVF 317
DB 252 LVFYVPGIFSLTHRGHHVPHHVVHLLATRYLLMPPALNPVYGVKTKQIRKRVVRVF 310

RESULT 3

OYJ3_HUMAN STANDARD; PRT; 311 AA.
AC Q8NH60;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 52J3.
GN OR52J3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Teutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
receptor genes";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);
CC


```

CC CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&
CC CC -----
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CC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC or send an email to license@isb-sib.ch).
CC CC -----
DR EMBL; AB065530; BAC05777.1; -.
DR Genew; HGNC:14799; OR52J3.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 48 1 (POTENTIAL).
FT DOMAIN 49 56 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 57 77 2 (POTENTIAL).
FT DOMAIN 78 101 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 102 122 3 (POTENTIAL).
FT DOMAIN 123 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 162 4 (POTENTIAL).
FT DOMAIN 163 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 238 6 (POTENTIAL).
FT TRANSMEM 239 259 7 (POTENTIAL).
FT DOMAIN 260 274 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 275 295 7 (POTENTIAL).
FT DOMAIN 296 311 CYTOPLASMIC (POTENTIAL).
FT DISULFID 99 191 BY SIMILARITY.
FT CARBOHYD 5 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 311 AA; 35060 MW; 73BBB0EE3102028 CRC64;

Query Match 52.6%; Score 904; DB 1; Length 311;
Best Local Similarity 54.3%; Pred. No. 2.3e-64;
Matches 169; Conservative 54; Mismatches 82; Indels 6; Gaps 2;

Qy 7 HNMESPHRTDVPVSFFLLGIPGLQFHLWLSLPVCGGLGTATVGNITILVVVATEPVLH 66
Db 4 HNKGFH-----PVTFLLGIPGLQFHLWLSLPVCGGLGTATVGNITILVVVATEPVLH 58
Qy 67 KPVLFLCMLSTIDLAASVSTPKLLAIFWCGAGHISASACLAHFFFIHAFQMESTVLL 126
Db 59 EPMFYLAULTIDLAASVSTPKLLAIFWCGAGHISASACLAHFFFIHAFQMESTVLL 118
Qy 127 AMAFDRYVAICHLRYATILDTTIAHIGVAAVVRGSLMLPCPFFIGRLNFCQSHVILH 186
Db 119 AMAFDRYVAICHLRYATILDTTIAHIGVAAVVRGSLMLPCPFFIGRLNFCQSHVILH 178
Qy 187 TYCHEMAVVKUACGTRPNRVYGTALLLVGVDFICGLSYALTAQAVRLSSHEARSK 246
Db 179 SYCHEMGIKLSGCGNIRINGIYGLFVVSFFV-LNLVLIGISYVILRAVFLPSHDAQLK 237
Qy 247 ALGTCGSHVCVILLISYTPALSFTHRGHHVPHVHILLANVLLPPALNPVYGVKT 306
Db 238 ALSTCGAHGVGVICFYIPSVFSFLTRFHQIPGVIHILVANVLLIIPSLNPIYGVRT 297
Qy 307 KQIRKRVVRVF 317
Db 298 KQIRVRLVVF 308

RESULT 4
ID_OYD1 HUMAN STANDARD; PRT; 318 AA.
AC Q9H346;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)

```

Olfactory receptor 52D1 (HORS'beta14).

OR52D1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20570519; PubMed=11121057;

RA Bulger M., Bender M.A., van Doorninck J.H., Wertman B., Farrell C.M.,

RA Felsenfeld G., Groudine M., Hardison R.,

RT "Comparative structural and functional analysis of the olfactory

RT receptor genes flanking the human and mouse beta-globin gene

RT clusters."

RL Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565 (2000).

CC -!- FUNCTION: Putative odorant receptor.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC -!- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);

CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol&

CC -----

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CC -----

CC EMBL; AF137396; AAG41676.1; --

CC Genew; HGNC:15212; OR52D1.

CC GO; GO:0016021; C: integral to membrane; NAS.

CC GO; GO:0004984; F: olfactory receptor activity; NAS.

CC GO; GO:0007608; P: olfaction; NAS.

CC InterPro; IPR000276; GPCR_Rhodpsn.

CC Pfam; PF00001; 7tm.1; 1.

CC PRINTS; PR00237; GPCRHOOPS.

CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.

CC PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.

CC G-protein coupled receptor; Transmembrane; Glycoprotein;

CC Multigene family; Olfaction.

FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 29 49 1 (POTENTIAL).

FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 58 78 2 (POTENTIAL).

FT DOMAIN 79 102 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 103 123 3 (POTENTIAL).

FT DOMAIN 124 142 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 143 163 4 (POTENTIAL).

FT DOMAIN 164 199 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 200 220 5 (POTENTIAL).

FT DOMAIN 221 240 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 241 261 6 (POTENTIAL).

FT DOMAIN 262 277 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 278 298 7 (POTENTIAL).

FT DOMAIN 299 318 CYTOPLASMIC (POTENTIAL).

FT DISULFID 100 192 BY SIMILARITY.

FT CARBOHYD 5 N-LINKED (GLCNAC...) (POTENTIAL).

SQ SEQUENCE 318 AA; 35121 MW; 178968087D613CB2 CRC64;

Query Match

Best Local Similarity 51.8%; Score 889.5; DB 1; Length 318;

Matches 160; Conservative 51; Mismatches 92; Indels 1; Gaps 1;

Qy 19 PSVFFLLGIPGLQFHLWLSLPVCGGLGTATVGNITILVVVATEPVLHKKPVFLCMLST 78

Db 12 PTFVFLTGIPGLQFHLWLSLPVCGGLGTATVGNITILVVVATEPVLHKKPVFLCMLST 71

Qy 79 IDLAASVSTVPKLLAIFWCGAGHISASACLAHFFFIHAFQMESTVLLAMAFDRYVAICH 138

Db 72 TDLALSSTVTPKMLAIFWCGAGHISASACLAHFFFIHAFQMESTVLLAMAFDRYVAICH 131

Qy 139 PLRYATILTDTTIAHIGVAAVVRGSLMLPCPFFIGRLNFCQSHVILHITYCHEMAVVKLA 198

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132 PLYRTTLNHAIVGRIGVGFGRSVAVSPFIPLRLRRPYCHRWVTHYCEHMGARLA 191
QY 199 CGDTRPNRVYGLTAAIIIVIGDLCIGLSYALIAQAVALRLSSHEARSKALGTGSHVCV 258
Db 192 CANITVNIVYGLTAVALLAGLDSILJASYGFILHAVFHLPSHDAQHAKALSTCGSHIG 251
QY 259 LISYTPALFSPFTHRFHGH-VPVHIHILLANVYLLPPALNPVVYGVTKQIRKVRVVF 317
Db 252 LVFYTPAFPSFTHRFHGHVPHVIFLANLYLVLPVLPNPLIYGARTKEIRSLKLL 311
QY 318 QSQG 321
Db 312 HLKG 315

RESULT 5
OYN4 HUMAN
ID OYN4 HUMAN STANDARD; PRT; 321 AA.
AC Q8NGI2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 52N4.
GN OR52N4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RA "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols";
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EMBL; AB065813; BAC06032.1; -
DR Genew; HGNC:15230; OR52N4.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00621; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 48 1 (POTENTIAL).
FT DOMAIN 49 56 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 57 77 2 (POTENTIAL).
FT DOMAIN 78 101 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 102 122 3 (POTENTIAL).
FT DOMAIN 123 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 162 4 (POTENTIAL).
FT DOMAIN 163 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 219 5 (POTENTIAL).
FT DOMAIN 220 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 260 6 (POTENTIAL).
FT DOMAIN 261 276 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 277 297 7 (POTENTIAL).

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FT DOMAIN 298 321 CYTOPLASMIC (POTENTIAL).
FT DISULFID 99 191 BY SIMILARITY.
FT CARBOHYD 5 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 321 AA; 36005 MW; A68363F08E3BA65C CRC64;
Query Match 51.5%; Score 885.5; DB 1; Length 321;
Best Local Similarity 52.6%; Pred. No. 6.9e-63;
Matches 162; Conservative 51; Mismatches 94; Indels 1; Gaps 1;
QY 15 TDVPSVFLLGIFGLFQFHLWLSLPVCGGLGTATVIGNITILVVVATEPVLHKPVYFLC 74
Db 7 TDLTPASFILNGVPLEDTQLWISFPFCGSMVYVAVMGNCGLLYLTHYEDALHKPMYFLA 66
QY 75 MLSTIDLAASVSTVPKLAIFWCAGHJISASACLAHMFIFHAFQWMSVESTVLLAMAFDRV 134
Db 67 MLSFTDLVMCSSTIPKALCIFWHLKDIQFDECLVQMFIFHTFTQMSGVLMLMALDRV 126
QY 135 AICHELRYATILTDITIAHIGVAAVVRGSLMLPCPFFIGRINFCQSHVILHYCEHMAV 194
Db 127 AICYPELRYSTILTNPVIAKVGATATFLRGVLLIIPFTLTKRLPYCRGNILPHTYCDHMSV 186
QY 195 VKLACGDTNRPNRVYGLTAAIIIVIGDLCIGLSYALIAQAVALRLSSHEARSKALGTGSH 254
Db 187 AKLSCGNVKNVAYGLMVALIIGGFIDILCITISYTMILRAVVVLSADARQAFNTCTAH 246
QY 255 VCVILISVTPALFSPFTHRFHGH-VPVHIHILLANVYLLPPALNPVVYGVTKQIRKV 313
Db 247 ICATVFTPTAPFSPFTHRFHGHIPPSCHIIVANVYLLPFTMPNIVYGVTKQIRDCV 306
QY 314 VRVFSQSQ 321
Db 307 IRILSGSK 314

RESULT 6
OYL2 HUMAN
ID OYL2 HUMAN STANDARD; PRT; 304 AA.
AC Q8NGH6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 52L2.
GN OR52L2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RA "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols";
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-----
EMBL; AB065820; BAC06039.1; ALT_INIT.
DR Genew; HGNC:14788; OR52L2.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

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DR PROSITE; PS0262; G PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 29 49 1 (POTENTIAL).
FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 58 78 2 (POTENTIAL).
FT DOMAIN 79 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 123 3 (POTENTIAL).
FT DOMAIN 124 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 163 4 (POTENTIAL).
FT DOMAIN 164 199 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 200 220 5 (POTENTIAL).
FT DOMAIN 221 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 261 6 (POTENTIAL).
FT DOMAIN 262 276 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 277 297 7 (POTENTIAL).
FT DOMAIN 298 304 CYTOPLASMIC (POTENTIAL).
FT DISULFID 100 192 BY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 304 AA; 33470 MW; 742CD45420A25A4D CRC64;

Query Match 51.4%; Score 883.5; DB 1; Length 304;
Best Local Similarity 57.7%; Pred. No. 9.5e-63;
Matches 169; Conservative 46; Mismatches 77; Indels 1; Gaps 1;

QY 19 PSVFFLLGIPGLEQPHLMSLPVCGLGTATVGNITILVVVATEPVVLPKPVYLFICMLST 78
DB 13 PS-FFLVGLPGLEESQHWLPALEGLYLLALVGNVTILFIIMDPSPHQSYFLSLMLAA 71
QY 79 IDLAASVSTVPKLLAIFWCGAGHISASACLAHMFHAFCMESTVLLAMAFDRYVAICH 138
DB 72 IDLVASSTAPKALAVLLVRAQEIQVTVCLIQMFTHAFSSNESGVLMALDRYVAICH 131
QY 139 PLRYATILDTIIAHIGVAAVVRGSLMLPCPFFIGRLNFCQSHVILHTYCEHMAVVKLA 198
DB 132 PLHHSTILHPGVIGHGMVLRGLLLIPELILKRLKIFQATIIIGHAYCEHMAVVKLA 191
QY 199 CGDTRPNRVYGLTALLVIGDLCIGLSYALIAQAVLRSLSHSARSALGTGCGSHVCV 258
DB 192 CSETTVNRYGLTVALLVGLVLAIGVSYAHILQAVLKVPNGEARLKAFSTGCGSHVCV 251
QY 259 LIISYTPALPFFTHFRGHVPHVHILLANVYLLPPLNVPVYGVKTKQIRK 311
DB 252 LVFIYIPGWFSLTHFRGHVPHVHILLALYRLVPLNVPVYGVKTKQIRK 304

RESULT 7
OYK1 HUMAN
ID OYK1 HUMAN STANDARD; PRT; 314 AA.
AC Q8NGK4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 52K1.
GN OR52K1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.,
FT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol
CC -----

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DR EMBL; AB065790; BAC06009.1; --
DR Genew; HGNC:15222; OR52K1.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1.
DR PROSITE; PS00337; G-PROTEIN RECP F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 48 1 (POTENTIAL).
FT DOMAIN 49 56 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 57 77 2 (POTENTIAL).
FT DOMAIN 78 101 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 102 122 3 (POTENTIAL).
FT DOMAIN 123 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 162 4 (POTENTIAL).
FT DOMAIN 163 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 219 5 (POTENTIAL).
FT DOMAIN 220 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 260 6 (POTENTIAL).
FT DOMAIN 261 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 296 7 (POTENTIAL).
FT DOMAIN 297 314 CYTOPLASMIC (POTENTIAL).
FT DISULFID 99 191 BY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 314 AA; 35289 MW; 8045963357FAB634 CRC64;

Query Match 51.3%; Score 881.5; DB 1; Length 314;
Best Local Similarity 53.2%; Pred. No. 1.4e-62;
Matches 167; Conservative 49; Mismatches 93; Indels 5; Gaps 1;

QY 5 LGHNHSEPHDTPSPVFFLLGIPGLEQPHLMSLPVCGLGTATVGNITILVVVATEPV 64
DB 2 LPSNITSTH-----PAVELLVIGIPGLEHLMHAWISIPFCFAYTLALLGNCTLLFIIRADA 56
QY 65 LHKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFHAFCMESTV 124
DB 57 LHPEWYFLAMLATIDLVLSSTILPKMLAIFWFRDQEIINFACLVQMFFLHSFSSMESAV 116
QY 125 LLAMAFDRYVAICHPLRYATILDTIIAHIGVAAVVRGSLMLPCPFFIGRLNFCQSHVI 184
DB 117 LLAMAFDRYVAICKELHYTTVLTGSLITKIGMAAVAWAVTLMPLPFLRRFHYCRGPVI 176
QY 185 LHTYCEHMAVVKLACGDTPRPNRVYGLTAAALVIGDLCIGLSYALIAQAVLRSLSHS 244
DB 177 AHYCEHMAVVRACGDTSPFNVIAGIYAVMEIVVLDLLFVLSVFILOVQLASQAR 236
QY 245 SKALGTGSHVCVILISYTPALPFFTHFRGHVPHVHILLANVYLLPPLNVPVYGV 304
DB 237 YKARFTCVSHIGAILSTYTPVWISSVMHVARHAPRVHILLAFIYLLFPWVNPVIYGV 296
QY 305 KTKQIRKRVVRVQ 318
DB 297 KTKQIRYVLSLFQ 310

RESULT 8
OYNS HUMAN
ID OYNS HUMAN STANDARD; PRT; 324 AA.
AC Q8NH56;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 52N5.
GN OR52N5.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Putami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RL receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols&
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB065535; BAC05781.1; -.
DR Genew; HGNC:15231; ORS2N5.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Multigene family;
KW Olfaction.
FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 54 1 (POTENTIAL).
FT DOMAIN 55 62 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 63 84 2 (POTENTIAL).
FT DOMAIN 85 108 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 109 129 3 (POTENTIAL).
FT DOMAIN 130 148 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 149 169 4 (POTENTIAL).
FT DOMAIN 170 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 226 5 (POTENTIAL).
FT DOMAIN 227 246 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 247 267 6 (POTENTIAL).
FT DOMAIN 268 283 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 284 304 7 (POTENTIAL).
FT DOMAIN 305 324 CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 198 BY SIMILARITY.
FT SEQUENCE 324 AA; 36226 MW; A060EA2FBSA5B792 CRC64;
Query Match 50.8%; Score 873; DB 1; Length 324;
Best Local Similarity 53.2%; Pred. No. 6.8e-62;
Matches 165; Conservative 52; Mismatches 91; Indels 2; Gaps 2;
QY 17 VDPSPVFLGIGLGFHWSLSPVCGLGTAIVGNITLVVATPEVLVHKPYFL-CM 75
Db 15 VTPSPFLGIGLGFHWSLSPVCGLGTAIVGNITLVVATPEVLVHKPYFL 74
QY 76 LSTIDLAASVSTPKLALFWCAGAGHSASACLAHMFHFAFCMESTVLLAMAFDRYVA 135
Db 75 LSLIDLTTCTTLPNALCFWLSKELNFAACLAQMFVHGFVGVSGVLMALDRYIA 134
QY 136 ICHPLRYATILDTTIAHGAIVVRSGLLMLPCPFIFGRNLNFCQSHVILHTYCEHMAVV 195
Db 135 ICYPLRYATLTNPILAKAELATFLRGVLIMIPPELVKRLPPCQSNILSHTYCDHMSVV 194
QY 196 KLAGCTRNRYVGLTAALLVIGVDLFCGLSVALIAQVLRLLSSHEARSKALGTCGSHV 255
Db 195 KLSCAIKNVYGLMVALVIGVDLFCGLSVALIAQVLRLLSSHEARSKALGTCGSHV 254
QY 256 CVILISVTPALPFFTHRF-GHVPVPHIILLANVYLLPPALNPVYGVKTKQIRKRVV 314
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Db 255 SALLITYPAFTFAHFGGHTTPPSLHIIVANLYLLPTLNPVYGVKTKQIRKSVI 314
QY 315 RVFSGQGQGWG 324
Db 315 KFFQDGKGGAG 324
RESULT 9
OXE2 RAT STANDARD; PRT; 320 AA.
AC O88628;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Olfactory receptor 51E2 (G-protein coupled receptor RALC).
GN OR51E2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99131082; PubMed=9932290;
RA Raming K., Konzelmann S., Breer H.;
RT "Identification of a novel G-protein coupled receptor expressed in
RT distinct brain regions and a defined olfactory zone.";
RL Recept. Channels 6:141-151(1998).
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed only in some areas of the brain and
CC in the olfactory epithelium.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF079864; AAD12761.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 25 45 1 (POTENTIAL).
FT DOMAIN 46 53 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 54 74 2 (POTENTIAL).
FT DOMAIN 75 98 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 99 119 3 (POTENTIAL).
FT DOMAIN 120 138 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 139 159 4 (POTENTIAL).
FT DOMAIN 160 195 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 196 216 5 (POTENTIAL).
FT DOMAIN 217 236 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 237 257 6 (POTENTIAL).
FT DOMAIN 258 272 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 273 293 7 (POTENTIAL).
FT DOMAIN 294 320 CYTOPLASMIC (POTENTIAL).
FT DISULFID 96 178 BY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GLCNAC...) (POTENTIAL).
FT SEQUENCE 320 AA; 35505 MW; E7FF78F5F5B9F94 CRC64;
Query Match 50.7%; Score 871; DB 1; Length 320;
Best Local Similarity 53.6%; Pred. No. 9.6e-62;
Matches 165; Conservative 49; Mismatches 94; Indels 0; Gaps 0;
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10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
DE Olfactory receptor 51E1.
DN OR51E1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsuchi S., Aburatani H., Asai K., Akiyama Y.,
RT "genome-wide discovery and analysis of human seven transmembrane helix
RL receptor genes";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Lung;
RC MEDLINE=22388257; PubMed=12477932;
RX Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.C., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Tothiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -I- FUNCTION: Putative odorant receptor.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -I- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols-

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CC or send an email to license@isb-sib.ch).

CC EMBL; AB065787; BAC06006.1; -
DR EMBL; BC022401; AAH22401.1; -
DR Genew; HGNC:15194; OR51E1.
DR InterPro; IPR000276; GPCR_Rhodpen.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GFCRRHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1.1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1.2; 1.
KW G-protein coupled receptor; transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 48 1 (POTENTIAL).
FT DOMAIN 49 56 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 57 77 2 (POTENTIAL).
FT DOMAIN 78 101 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 102 122 3 (POTENTIAL).
FT DOMAIN 123 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 162 4 (POTENTIAL).
FT DOMAIN 163 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 219 5 (POTENTIAL).

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DR EMBL; AB065816; BAC06035.1; -.
DR Genew; HGNC:15228; OR52N2.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G PROTEIN RECP Fl_1; 1.
DR PROSITE; PS0262; G PROTEIN RECP Fl_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 48 1 (POTENTIAL).
FT DOMAIN 49 56 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 57 77 2 (POTENTIAL).
FT DOMAIN 78 101 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 102 122 3 (POTENTIAL).
FT DOMAIN 123 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 162 4 (POTENTIAL).
FT DOMAIN 163 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 219 5 (POTENTIAL).
FT DOMAIN 220 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 260 6 (POTENTIAL).
FT DOMAIN 261 276 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 277 297 7 (POTENTIAL).
FT DOMAIN 298 321 CYTOPLASMIC (POTENTIAL).
FT DISULFID 99 191 BY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 321 AA; 35940 MW; A08A2658BD26477C CRC64;

Query Match      49.0%; Score 842; DB 1; Length 321;
Best Local Similarity 48.6%; Pred. No. 1.9e-59;
Matches 156; Conservative 62; Mismatches 97; Indels 6; Gaps 2;

QY 9 MESPHTDVPSPVFFLLGIPGLEQFHLWLSLPCVGLGTATVGNITILVVVATEPVVHKP 68
Db | : : : | | | : | | : | : | : | : | : | : | : | : | : | : |
1 MSGDNSSSLTPGFFILNGVGELEATHIWISLPFCFMYIIAVVGVNCGLCGLISHEEALHRP 60
QY 69 VYLFCLMLSTIDLAASVTVPKLALFWCGAGHISASACLAHMFTHAFCMVESTVLLAM 128
Db | : : : | | : | | : | | : | | : | | : | | : | | : | | : |
61 MYVFLALLSFTDVLCTVNPVNMCLIFWENLKEIDFNACLAQMFVHMLTGMESGVMLM 120
QY 129 ADRVVAICHPLRYATILDTTIAHIGVAAVVRGSLMLPCPFFIGRLNFCQSHVILHTY 188
Db | : : : | | : | | : | | : | | : | | : | | : | | : | | : |
121 ALDRYVAICYPLRYATILNPNVIKAGLATFLRNVMLIIPFTLLTKRLPYCRGNFIPHTY 180
QY 189 CEHMAVVKLACGDTREPNVYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSSHEARSKAL 248
Db | : : : | | : | | : | | : | | : | | : | | : | | : | | : |
181 CDHMSVAKVSCGNFKVNAIYGLMVALLIGVFDICCSVSYTMLQAVMSLSSADARHKAF 240
QY 249 GTCGSHVCVILISYTPALPFFTHRF-GHHVPVHIHILLANVYLLPPALNPVYGVKTK 307
Db | : : : | | : | | : | | : | | : | | : | | : | | : | | : |
241 STCTSHMCSIVITYVAAAFPTFTTHRFVGHNIHNIHIIIVANLYLLPPTMNFIVGVKTK 300
QY 308 QIRKRVVRVFGSQGGMGIKAS 328
Db | : : | : |
301 QIQEGVIRKFL-----LGDKVS 316
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Search completed: September 15, 2004, 21:36:39
Job time : 14 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 21:34:03 ; Search time 44 Seconds
(without alignments)
2359.216 Million cell updates/sec

Title: US-10-081-775-2
Perfect score: 1718
Sequence: 1 MSSTLGHNMESPHHTDVPDPS.....RKVVVVFQSGQGMKIKASE 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1534	89.3	329	11	Q8VGX9
2	1517	88.3	321	11	Q7TRP8
3	977.5	56.9	315	11	Q8VG23
4	936.5	54.5	299	4	Q8NGF2
5	936	54.5	316	11	Q7TRN7
6	927	54.0	317	11	Q8VGX8
7	912.5	53.1	319	11	Q7TRS6
8	907.5	52.8	317	11	Q8VEX9
9	891.5	51.9	311	11	Q7TRR4
10	891.5	51.9	317	11	Q8VGW8
11	890.5	51.8	323	11	Q8VGW5
12	890	51.8	314	11	Q8V3Z2
13	890	51.8	318	11	Q8VGA1
14	887.5	51.7	316	11	Q8VG79
15	887.5	51.7	318	11	Q8VGW3
16	887.5	51.7	326	11	Q9WVD9

17	883.5	51.4	317	11	Q8VGU9	Q8vgu9 mus musculu
18	883	51.4	316	11	Q7TRRS	Q7trrs mus musculu
19	883	51.4	327	11	Q8VF28	Q8vf28 mus musculu
20	883	51.4	339	11	Q9WU90	Q9wu90 mus musculu
21	882.5	51.4	312	11	Q8VGW2	Q8vgw2 mus musculu
22	881.5	51.3	317	11	Q8VH04	Q8vh04 mus musculu
23	880.5	51.3	312	11	Q7TRR6	Q7trr6 mus musculu
24	877.5	51.1	316	11	Q7TRQ8	Q7trq8 mus musculu
25	877.5	51.0	341	11	Q8VF27	Q8vf27 mus musculu
26	875	50.9	314	11	Q7TRR0	Q7trr0 mus musculu
27	873.5	50.8	312	11	Q8VGX4	Q8vgx4 mus musculu
28	873	50.8	317	11	Q8VG77	Q8vg77 mus musculu
29	871.5	50.7	316	11	Q8VG24	Q8vg24 mus musculu
30	871	50.7	319	11	Q8VG99	Q8vg99 mus musculu
31	871	50.7	324	11	Q7TRP9	Q7trp9 mus musculu
32	870	50.6	314	11	Q7TRS2	Q7trs2 mus musculu
33	868.5	50.6	312	11	Q8VF06	Q8vf06 mus musculu
34	868.5	50.6	319	11	Q8VGW0	Q8vgw0 mus musculu
35	867.5	50.5	314	11	Q7TRS0	Q7trs0 mus musculu
36	866	50.4	314	11	Q9EQ06	Q9eq06 mus musculu
37	865	50.3	316	11	Q8VH03	Q8vh03 mus musculu
38	865	50.3	320	11	Q8VBV9	Q8vbv9 mus musculu
39	864.5	50.3	312	11	Q7TRP3	Q7trp3 mus musculu
40	860.5	50.1	308	11	Q8VG84	Q8vg84 mus musculu
41	858	49.9	314	11	Q7TRR7	Q7trr7 mus musculu
42	854	49.7	314	11	Q8VEW8	Q8vew8 mus musculu
43	852	49.6	318	11	Q8VH00	Q8vh00 mus musculu
44	851.5	49.6	317	4	Q8NGK5	Q8ngk5 homo sapien
45	851	49.5	322	11	Q8VGW5	Q8vgw5 mus musculu

ALIGNMENTS

RESULT 1

Q8VGX9 PRELIMINARY; PRT; 329 AA.

AC Q8VGX9; 01-MAR-2002 (Tremblrel. 20, Created)

DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)

DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)

DE Olfactory receptor MOR27-1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1] SEQUENCE FROM N.A.

RA Zhang X., Firestein S.J.;

RT "The olfactory receptor gene superfamily of the mouse.";

RL Nat. Neurosci. 0:0-0(2002).

RN [2] SEQUENCE FROM N.A.

RA Adams M.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY073012; AAL60675.1; -

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001594; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm.1; 1.

DR PRINTS; PR00237; GPCR_Rhodopsn.

DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.

DR PROSITE; PS00262; G-PROTEIN-RECEPTOR FL2; 1.

KW Receptor.

SQ SEQUENCE. 329 AA; 36285 MW; 7D23203F650861BF CRC64;

Query Match 89.3%; Score 1534; DB 11; Length 329;
Best Local Similarity 88.1%; Pred. No. 8.8e-135;
Matches 290; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MSSTLGHNMESPHHTDVPDPSVFFLLGIPGLEQHLWLSLPVCGIGTATVGNITILVVA 60

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Db 1 MSNTSQWSPNHTDLPSTIFFLLGIPGLQFEMWLSLPVCCCLGTATIVGNITILVVVA 60
QY 61 TEPVLHKEVYLFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFHIFAFQCM 120
Db 61 TEPTLHRPVLFLCMLSTIDLAASVSTVPKLLAILWCAGHISASACLTQMFHIFAFQCM 120
QY 121 ESTVLLAMAFORYVAICHPLRYATILDTTIIAHIGVAAVVRGSLMLPCPFIFGLNFCQ 180
Db 121 ESTVLLAMAFORYVAICHPLRYATILDTTIIAHIGVAAVVRGSLMLPCPFIFGLNFCQ 180
QY 181 SHVILHTYCEHMAVVKACGDRPNRVVGLTAALVIGVDFLCGLSYALIAQAVALRLSS 240
Db 181 SHVILHTYCEHMAVVKACGDRPNRVVGLTAALVIGVDFLCGLSYALIAQAVALRLSS 240
QY 241 HEARSKALGTGSHVCVILISYTPALFSFFTHRFHGHVPHVHIHILLANVYLLPPALNPV 300
Db 241 HEARSKALGTGSHVCVILISYTPALFSFFTHRFHGHVPHVHIHILLANVYLLPPALNPV 300
QY 301 YGVKTKQIRKRVVRVFGSGQGMKASE 329
Db 301 YGVKTRERIRVAKVFGQGTRLKISK 329

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RESULT 2

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QYTRP8 PRELIMINARY; PRT; 321 AA.
ID Q7TRP8
AC Q7TRP8
DT 01-OCT-2003 (TREMELrel. 25, Created)
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Olfactory receptor GA_x6K02T2PB9-7245486-7246451.
GN GA_x6K02T2PB9-7245486-7246451.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA Walker M., Williams E.M., Axel R., Trask B.J.;
RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
RT genes, extensive alternate splicing, and unequal expression levels.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sanders K.;
RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY317777; AAP71129.1; -.
KW Receptor.
SQ SEQUENCE 321 AA; 35422 MW; 75B78779DEC4D0F CRC64;

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Query Match 88.3%; Score 1517; DB 11; Length 321;
Best Local Similarity 89.4%; Pred. No. 3.3e-133;
Matches 287; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

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QY 9 MESPHTDVPDPSVFFLLGIPGLEQFHLWLSLPCVGLGTATIVGNITILVVATEPVLHQP 68
Db 1 MESPHTDLPSTIFFLLGIPGLEQFHLWLSLPCVGLGTATIVGNITILVVATEPVLHQP 60
QY 69 VYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFHIFAFQCMESTVLLAM 128
Db 61 VYFLCMLSTIDLAASVSTVPKLLAILWCAGHISASACLTQMFHIFAFQCMESTVLLAM 120
QY 129 AFDYVAICHPLRYATILDTTIIAHIGVAAVVRGSLMLPCPFIFGLNFCQSHVILHTY 188
Db 121 AFDYVAICHPLRYATILDTTIIAHIGVAAVVRGSLMLPCPFIFGLNFCQSHVILHTY 180
QY 189 CEHMAVVKACGDRPNRVVGLTAALVIGVDFLCGLSYALIAQAVALRLSSHEARSKAL 248
Db 181 CEHMAVVKACGDRPNRVVGLTAALVIGVDFLCGLSYALIAQAVALRLSSHEARSKAL 240
QY 249 GTCGSHVCVILISYTPALFSFFTHRFHGHVPHVHIHILLANVYLLPPALNPVYGVKTKQ 308

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Db 241 GTCGSHVCVILISYTPALFSFFTHRFHGHVPHVHIHILLANVYLLPPALNPVYGVKTKRE 300
QY 309 IRKRVVRVFGSGQGMKASE 329
Db 301 IRERVAKVFGQGTRLKISK 321

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RESULT 3

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QYQV23 PRELIMINARY; PRT; 315 AA.
ID Q8VG23
AC Q8VG23;
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Olfactory receptor MOR29-1 (Olfactory receptor
DE GA_x6K02T2PB9-5307445-5306498).
GN GA_x6K02T2PB9-5307445-5306498.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RA "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA Walker M., Williams E.M., Axel R., Trask B.J.;
RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
RT genes, extensive alternate splicing, and unequal expression levels.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Sanders K.;
RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY073340; AAL61003.1; -.
DR EMBL; AY317664; AAP71043.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 315 AA; 34242 MW; 0926C74DB9A4470C CRC64;

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Query Match 56.9%; Score 977.5; DB 11; Length 315;
Best Local Similarity 56.4%; Pred. No. 6.1e-83;
Matches 176; Conservative 56; Mismatches 79; Indels 1; Gaps 1;

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QY 9 MESPHTDVPDPSVFFLLGIPGLEQFHLWLSLPCVGLGTATIVGNITILVVATEPVLHQP 68
Db 1 MQHTNHSHQNPSSFLLMGIPGLEASHFWIAFPFCSNYALAVLGNMAVLVVRSEPSLHQP 60
QY 69 VYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFHIFAFQCMESTVLLAM 128
Db 61 MYFLCMLSTIDLLCTSTVPKLLALFWANAELAFGACATQMFTHGFSAVESGLISM 120
QY 129 AFDYVAICHPLRYATILDTTIIAHIGVAAVVRGSLMLPCPFIFGLNFCQSHVILHTY 188
Db 121 AFDYVAICHPLRYGSLSSSESVSKLGAALLRGLGLMTPLTCLLARLSYC-GRVVAHSY 179
QY 189 CEHMAVVKACGDRPNRVVGLTAALVIGVDFLCGLSYALIAQAVALRLSSHEARSKAL 248

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Db 180 CEHMAVVKACGGTQPNNIYIGITATLVVGTSDICIAISYALILRAVLGLSSKEARAKTF 239
QY 249 GTCGSHVCVILSYITPALSFFTHRGHVPVHIHILLANVLLPPALNPVVGKTKQ 308
Db 240 GTCGSHLGVILLFYTPGLFSFTQRFQGVPRHVHILLADLYLVPPMLNPIYGMKTKQ 299
QY 309 IRKRVVRVFSQ 320
Db 300 IRDGALLRLKRG 311

RESULT 4
Q8NGF2 PRELIMINARY; PRT; 299 AA.
AC Q8NGF2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Seven transmembrane helix receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB065856; BAC06074.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1. 1.
DR PRINTS; PRO0237; GPCR_RHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 299 AA; 32514 MW; 5812D24DC8CD8F4A CRC64;

Query Match 54.5%; Score 936.5; DB 4; Length 299;
Best Local Similarity 58.4%; Pred. No. 3.8e-79;
Matches 173; Conservative 48; Mismatches 74; Indels 1; Gaps 1;

QY 25 LGIPGLEQFHLWLSLPVCGLTATVGNITILVWVATEPVLPKPVYFLCMLSTIDLAAAS 84
Db 1 MGIPGPEASHFWIAFPFCSMYALAVLGNMVLVHSEPVLPQPMYFLCMLSTIDLVLVC 60
QY 85 VSTVPKLLAIFWCGAGHISASACLAHMPFIHAFCMMESTVLLAMAFDRYVAICHPLRYAT 144
Db 61 TSTVPKLLALFWAKDAEINFGCAQMPFIHGFSAVESGILLAMAFDRYLAICPLPHYGS 120
QY 145 ILTDITLIIHIGVAAVVRGSLMLPCPFFTGRLNFCQSHVILTYCEHMAVVKACGDRP 204
Db 121 LLSPEVSKLGAVALRGLGLMTPLTCLLARLSYC-SRVVAHSYCEHMAVVKACGGTQP 179
QY 205 NRVIYGLTALLVIGVDLFCIGLSYALIAQAVLRLLSSHEARSKALGTGCGSHVCVILISYTP 264
Db 180 NNIIYGITATLVVGTSDICIAVSYALILRAVLGLSSKEARAKTFGCGSHLGVILLFYTP 239
QY 265 ALFSPFTHRGHVPVHIHILLANVLLPPALNPVVGKTKQIRKRVVRVFSQ 320
Db 240 GLFSFVTRFQGVPRHVHILLADLYLVPPMLNPIYGMKTKQIWDGALLKKG 295

RESULT 5
Q7TRN7 PRELIMINARY; PRT; 316 AA.
AC Q7TRN7;
ID Q7TRN7

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DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Olfactory receptor GA x6K02T2PBJ9-7810071-7809121.
GN GA_x6K02T2PBJ9-7810071-7809121.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
RA Walker M., Williams E.M., Axel R., Trask B.J.;
RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
RT genes, extensive alternate splicing, and unequal expression levels.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY317806; AAP71152.1; -.
KW Receptor.
SQ SEQUENCE 316 AA; 34759 MW; 471D578C6F5D6B4B CRC64;

Query Match 54.5%; Score 936; DB 11; Length 316;
Best Local Similarity 59.1%; Pred. No. 4.5e-79;
Matches 175; Conservative 46; Mismatches 75; Indels 0; Gaps 0;

QY 22 FELLGIPGLEQFHLWLSLPVCGLTATVGNITILVWVATEPVLPKPVYFLCMLSTIDL 81
Db 15 FLVGVPGLEESQHWIAPLGLIYLFALVGNVTIIIFIWTDSSLQPMYFLFLAMLAIDL 74
QY 82 AASVSTVPKLLAIFWCGAGHISASACLAHMPFIHAFCMMESTVLLAMAFDRYVAICHPLR 141
Db 75 VLASSTAPKALFVLLAHAHEIGYIVCLTQMFIHAFSSMESGILVAMALDRYVAICHPLR 134
QY 142 YATILTDITLIIHIGVAAVVRGSLMLPCPFFTGRLNFCQSHVILTYCEHMAVVKACGD 201
Db 135 HSTILHPGIIGRIGLVLRGLVLPFPFILLQNVVFCRATVISHAYCEHMAVVKACSE 194
QY 202 TRPNRVYGLTALLVIGVDLFCIGLSYALIAQAVLRLLSSHEARSKALGTGCGSHVCVILIS 261
Db 195 TTVNRAYGLSVALLVVDLVAIGISYALILQAVLKVPGEARLKAFSTCGSHVCVILIF 254
QY 262 YTPALFSPFTHRGHVPVHIHILLANVLLPPALNPVVGKTKQIRKRVVRVF 317
Db 255 YVPGMFSEFLTRFGHHVPHVHLLATLYLLVPPALNPVVGKTKQIRQVRVRF 310

RESULT 6
Q8VGX8 PRELIMINARY; PRT; 317 AA.
ID Q8VGX8
AC Q8VGX8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Olfactory receptor MOR33-1 (Olfactory receptor
DE GA_x6K02T2PBJ9-7206970-7207923).
GN GA_x6K02T2PBJ9-7206970-7207923.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]

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RN	[2]
RP	SEQUENCE FROM N.A.
RA	Sanders K.;
RL	Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AY317666; AAP71045.1; -.
KW	Receptor.
SQL	SEQUENCE 319 AA; 35259 MW; DB5D88EA93733128 CRC64;
Query Match	53.1%; Score 912.5; DB 11; Length 319;
Best local similarity	56.8%; Pred. No. 7.le-77;
Matches 172; Conservative 45; Mismatches 85; Indels 1; Gaps 1	
QY	19 PSVFLLGIPGLEQFHLWSLPVCGLGATTVGNITILVVATEPVLHKPVYFLCMLST 78
DB	11 PSEFWLTGIPGLESLSHMLSIPFGSMYLVAVGNITILLAVKTERSLQPWFYFLCMLAV 70
QY	79 IDLAASVSTVPKLAIATFCWGAGHSASACLAHMFFIHAFCMWESTVLLAMAFDRVAICH 138
DB	71 IDLVLSSTMPKLLAIFWFGACSIGLDACLQMFEFVCATVESGIFLAMAFDRVAICD 130
QY	139 PLRYATILTDTIIAHGVAAVVRGSLMLPCFFFI-PLNCOSHVILHTYCEHMAVVKL 197
DB	131 PLHHTSVLTHAVRGGLAALRGVYIGPLLIIRLRDLRPFRTQIIAHSYCEHMAVVTL 190
QY	198 ACGTRENRVYGLTAALLIVIGVDLFICGLSVALIAQAVALRLSSHEARSKALGTGSHVCV 257
DB	191 ACGDTKNVLYGMGIGFVLILDIAITASYIMIFRAVLGLSTSDARFKTLTCGSHICA 250
QY	258 ILSYTFALSFFFHRGHVPHVIHILLANVYILLPALNPVVGVTKOIRKRVRVRF 317
DB	251 ILVEYIPIAVSSLTRFHGNVPSHIILLANFYLLIPPILNPVVYAVRTKQIRERLLHII 310
QY	318 QSG 320
DB	311 XSG 313
RESULT 8	
ID	QBVEIX9 PRELIMINARY; PRT; 317 AA.
AC	QBVEIX9;
DT	01-MAR-2002 (TREMBLrel. 20, Created)
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Olfactory receptor MOR25-1 (Olfactory receptor
DN	GA_X6K02t2PB39-5356887-5357840).
GN	GA_X6K02t2PB39-5356887-5357840.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCHI_TaxID=10090;
[1]	-
RP	SEQUENCE FROM N.A.
RA	Zhang X., Firestein S.J.;
RT	"The olfactory receptor gene superfamily of the mouse.";
RL	Nat. Neurosci. 0:0-0(2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Adams M.;
RL	Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR	[3]
RP	SEQUENCE FROM N.A.
RA	Young J.M., Shykind B.M., Lane R.P., Tonnes-Friddy L., Ross J.A.,
RA	Walker M., Williams E.M., Axel R., Trask B.J.;
RT	"Odorant receptor ESTs demonstrate olfactory expression of over 400
RT	genes, extensive alternate splicing, and unequal expression levels.";
RL	Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN	[4]
RP	SEQUENCE FROM N.A.
RA	Sanders K.;
RL	Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AY073768; AAL61431.1; -.
DR	EMBL; AY317667; AAP71046.1; -.

DR GO: 0016021; C: integral to membrane; IEA.
 DR GO: 0004872; F: receptor activity; IEA.
 DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO: 0007186; P: G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 317 AA; 34969 MW; 098189C67F91DB8E CRC64;

Query Match 52.8%; Score 907.5; DB 11; Length 317;
 Best Local Similarity 55.9%; Pred. No. 2.1e-76;
 Matches 175; Conservative 45; Mismatches 92; Indels 1; Gaps 1;

QY 9 MESPHTDVPDPVFFLLGIGLQFHLWLSLPVCGGLGTATVIGNITILVVVATEPVLHKP 68
 Db 1 MSTFHNVCSPSSLLWTGIPGLETLHLSIPFGSMYLVAVGNTITILAVRVERSLHQ 60
 QY 69 VYLFCLMSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHFFFIHAFCMESTVLLAM 128
 Db 61 MYFFLCMLAVIDLVLSITMPKLLAIFWFGAGHIGDACLQMLIHCFATVSGIFLAM 120
 QY 129 AFDYVAICHPRYATILDTTIIAHGVAAVVRGSLMLPCPPFFIG-RLNFCQSHVILHT 187
 Db 121 AFDYVAICNPLRHSMVLTHTLVGRGLAAVLGRVYIGPLMIRLRLPLYKTRVISHS 180
 QY 188 YCEHMAVVKLACGTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRSLSSHEARSKA 247
 Db 181 YCEHMAVVALTCGDSRVNNVYIGSLFGLVLIDSAATAASYVMIFRAVWGLATPEARLKA 240
 QY 248 LGTCGSHVCVILISYTPALFSPFTHRGHVPVHIHLLANVLLPPALNPVYGVKTK 307
 Db 241 LGTCGSHICALLFYPIAVSSLIHRFGHQVPPPIHTLLANFYLPIILNPVIVAVRTK 300
 QY 308 QIRKRVVRVQSG 320
 Db 301 QIRDRLQLKLTG 313

RESULT 9
 Q7TRR4 PRELIMINARY; PRT; 311 AA.
 ID Q7TRR4;
 AC Q7TRR4;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DE Olfactory receptor MOR32-3 (Olfactory receptor)
 DE GA_X6K02T2PB9-5935234-5936169.
 GN GA_X6K02T2PB9-5935234-5936169.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1] SEQUENCE FROM N.A.
 RP Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
 RA Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 RT genes, extensive alternate splicing, and unequal expression levels."
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [2] SEQUENCE FROM N.A.
 RP Sanders K.;
 RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY317709; AAP1076.1; -;
 KW Receptor.
 SQ SEQUENCE 311 AA; 35111 MW; AF0317C0147D261C CRC64;

Query Match 51.9%; Score 891.5; DB 11; Length 311;
 Best Local Similarity 56.4%; Pred. No. 6.2e-75;
 Matches 171; Conservative 46; Mismatches 85; Indels 1; Gaps 1;

QY 15 TDVDPVSFLLGIPGLEQFHLWLSLPVCGGLGTATVIGNITILVVVATEPVLHKPVLFLC 74

Db 7 TQHPSSFLLLGIPGLESHHTWIGFPFCAYLIALGNFTILLVIKTESLHQPMFYFLA 66
 QY 75 MLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHFFFIHAFCMESTVLLAMAFDRYV 134
 Db 67 MLATIDLGLSTATIPKMLGIFWFSRVLLFGACLTQMFIIHNF7GMSAVLLAMAYDRYV 126
 QY 135 AICHPLRYATILDTTIIAHGVAAVVRGSLMLPCPPFFIGRLNFCQSHVILHTYCEHMAV 194
 Db 127 AICNPLRYSTILTAKAVFMIGLVYRSLVSPFFFLILRLPFCGNNVLPHYICEHML 186
 QY 195 VKLACGTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRSLSSHEARSKALGTCSH 254
 Db 187 ARUSCANIKVNIYGL-GAISILFDDIIAIALSYAQILRAVFLRPREARIKSILSTCSH 245
 QY 255 VCVILISYTPALFSPFTHRGHVPVHIHLLANVLLPPALNPVYGVKTKOIRKRV 314
 Db 246 VCVILAFYTPALFSPFTHRGHVPVHIHLLANVLLPPALNPVYGVKTKOIRKRV 305
 QY 315 RVF 317
 Db 306 KIF 308

RESULT 10

Q8VGV8 PRELIMINARY; PRT; 317 AA.
 ID Q8VGV8;
 AC Q8VGV8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE Olfactory receptor MOR32-3 (Olfactory receptor)
 DE GA_X6K02T2PB9-5871256-5870303.
 GN GA_X6K02T2PB9-5871256-5870303.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1] SEQUENCE FROM N.A.
 RP Zhang X., Firestein S.J.;
 RA "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2] SEQUENCE FROM N.A.
 RP Adams M.;
 RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3] SEQUENCE FROM N.A.
 RP Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
 RA Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 RT genes, extensive alternate splicing, and unequal expression levels."
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4] SEQUENCE FROM N.A.
 RP Sanders K.;
 RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY073036; AAL60699.1; -;
 DR EMBL; AY317704; AAP1072.1; -;
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 317 AA; 36135 MW; 637560B054F48AC8 CRC64;

Query Match 51.9%; Score 891.5; DB 11; Length 317;
 Best Local Similarity 54.0%; Pred. No. 6.4e-75;

Matches 168; Conservative 49; Mismatches 93; Indels 1; Gaps 1;

QY 12 PHHTDVSFFLLGIPGLQFLMLSLPVCGLGATIVGNITILVWVATEPVLKHPVL 71
 DB 4 PNDTQFHSFTLLGIPGLQFLMLSLPVCGLGATIVGNITILVWVATEPVLKHPVL 63

QY 72 FICMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFTHAFCMESTVILLAM 131
 DB 64 FLAMLATIDGLSTATIPKMLGIFWNLREILFEDCLIQMFIHFKFTLMESTVILLAM 123

QY 132 RVAICHPLRYATILDTIIAHIGVAAVVRGSLMLPCPFIFGRMLNFCOSHVILHTY 191
 DB 124 HVAICIPURYSTILNPKVSMIGIAVLRAIFVIPPFLILRLDPFCGHIIPIPHYCH 183

QY 192 MAVVKIACGDTTRPNRVYGLTAALLVIGDLFCIGLSYALIAQAVALRSLSHEARS 251
 DB 184 MGLARLSCASVKANVIYGLCAICNLL-FDVAIVLSYIQILRVVFLPAREARLSLNTC 242

QY 252 GSHVCVILSYTPALFSPFTHRGHVPVHIHILLANVLLPPALNPVYGVKTKQIRK 311
 DB 243 GSHVCVILAFYTPALFSPFTHRGHVPVHIHILLANVLLPPALNPVYGVKTKQIRK 302

QY 312 RVVRVFSQSG 322
 DB 303 RVKILLQVRG 313

RESULT 11

ID Q8VGVS PRELIMINARY; PRT; 323 AA.

AC Q8VGVS;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Olfactory receptor MOR34-5 (Olfactory receptor
 DE GA_X6K02T2PB39-7273558-7272587).
 GN GA_X6K02T2PB39-7273558-7272587.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
 RA Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 RT genes, extensive alternate splicing, and unequal expression levels."
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY073039; AAL60702.1; -.
 DR EMBL; AY317779; AAP71131.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.

SQ SEQUENCE 323 AA; 36060 MW; 84FE6A4B4978C936 CRC64;

Query Match 51.8%; Score 890.5; DB 11; Length 323;
 Best Local Similarity 52.5%; Pred. No. 8.1e-75;
 Matches 165; Conservative 52; Mismatches 96; Indels 1; Gaps 1;

QY 9 MESPHHTDVSFFLLGIPGLQFLMLSLPVCGLGATIVGNITILVWVATEPVLKHP 68
 DB 3 MSVQNSTDLTPASFVINGIPGLQFLMLSLPVCGLGATIVGNITILVWVATEPVLKHP 62

QY 69 VYLFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFTHAFCMESTVILLAM 128
 DB 63 MYFLAMLSTLDLVNCSSTIPKTLCTFWFHLKEIGFDCLVQMFHTFTGMESGYMLM 122

QY 129 ADRVVAICHPLRYATILDTIIAHIGVAAVVRGSLMLPCPFIFGRMLNFCOSHVILHTY 188
 DB 123 ALDRVVAICHPLRYATILDTIIAHIGVAAVVRGSLMLPCPFIFGRMLNFCOSHVILHTY 182

QY 189 CEHMAVKIACGDTTRPNRVYGLTAALLVIGDLFCIGLSYALIAQAVALRSLSHEARS 248
 DB 183 CEHMSVAKLSCGNVKNVYGLVALLIGDFDILCITISYTMILRAVWSLSSADARQKAF 242

QY 249 GTCGSHVCVILSYTPALFSPFTHRGHVPVHIHILLANVLLPPALNPVYGVKTK 307
 DB 243 STCTAHICAIVFSYSPAFSFFSHRFGHTIPPSCHIIIVANILYLLPPTMNPVYGVKTK 302

QY 308 QIRKRVVRVFSQSG 321
 DB 303 QIRDCVIRILSGSK 316

RESULT 12

ID Q8VGZ2 PRELIMINARY; PRT; 314 AA.

AC Q8VGZ2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Olfactory receptor MOR30-1 (Olfactory receptor
 DE GA_X6K02T2PB39-5599295-5598351).
 GN GA_X6K02T2PB39-5599295-5598351.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Ross J.A.,
 RA Walker M., Williams E.M., Axel R., Trask B.J.;
 RT "Odorant receptor ESTs demonstrate olfactory expression of over 400
 RT genes, extensive alternate splicing, and unequal expression levels."
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Sanders K.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY072998; AAL60661.1; -.
 DR EMBL; AY317684; AAP71059.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.

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OM protein - protein search, using sw model

Run on: September 15, 2004, 21:32:48 ; Search time 57 Seconds
(without alignments)
1630.844 Million cell updates/sec

Title: US-10-081-775-2

Perfect score: 1718

Sequence: 1 MSSTLGHNMESPHHTDVPDPS.....RKRVVRVFSQSGCMKXASE 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1718	100.0	329	6 ABO42809	Abc42809 Human G-p
2	1691	98.4	329	4 AAU24646	Aau24646 Human Olf
3	1691	98.4	329	5 ABP51578	Abp51578 Human G p
4	1691	98.4	329	5 ABP51577	Abp51577 Human G p
5	1691	98.4	329	5 ABP95772	Abp95772 Human GPC
6	1691	98.4	329	5 AAU85266	Aau85266 G-coupled
7	1691	98.4	329	7 ADC86345	Adc86345 Human GPC
8	1649	96.0	321	4 AAG71674	Aag71674 Human Olf
9	1649	96.0	321	5 AAU80511	Aau80511 Human G-c
10	1649	96.0	321	5 AAU95725	Aau95725 Human Olf
11	1376	80.1	316	6 ABR01673	AbR01673 Human G p
12	972.5	56.6	329	4 AAG71876	Aag71876 Human Olf
13	950.5	55.3	316	6 ABR01670	AbR01670 Human G p
14	936.5	54.5	299	7 ADC86381	Adc86381 Human GPC
15	931.5	54.2	314	4 AAG72396	Aag72396 Human OR-
16	931.5	54.2	314	4 AAG71545	Aag71545 Human Olf
17	931.5	54.2	329	5 AAB71366	Aab71366 Human GCR
18	931.5	54.2	329	5 ABP95753	Abp95753 Human GPC
19	931.5	54.2	329	5 AAU95700	Aau95700 Human Olf
20	931.5	54.2	329	7 ADC86367	Adc86367 Human GPC
21	920	53.6	326	4 AAE06752	Aae06752 Human G-p
22	907	52.8	311	4 ABB44530	Abb44530 Human GPC
23	904	52.6	311	4 AAG71562	Aag71562 Human Olf
24	904	52.6	311	4 ABB44528	Abb44528 Human GPC
25	904	52.6	311	4 AAU10309	Aau10309 G-protein

ALIGNMENTS

RESULT 1

ABO42809
ID ABO42809 standard; protein; 329 AA.

XX AC ABO42809;

XX DT 22-SEP-2003 (first entry)

XX DE Human G-protein coupled receptor HGPRMY25.

XX KW Human; G-protein coupled receptor; HGPRMY25; immune disease;
KW inflammatory disease; arthritis; asthma; AIDS; psoriasis;
KW graft-versus-host disease; systemic lupus erythematosus;
KW reproductive disorder; varicocele; orchitis; neural disorder;
KW Alzheimer's disease; Parkinson's disease; depression; schizophrenia;
KW cardiovascular disorder; hypertension; acute heart failure;
KW pulmonary disorder; endocrine disorder; obesity; diabetes; anorexia;
KW bone disorder; osteoporosis; pain; cancer; chromosome identification;
KW gene therapy; receptor.
XX OS Homo sapiens.

XX PN US2003060409-A1.

XX PD 27-MAR-2003.

XX PF 21-FEB-2002; 2002US-00081775.

XX PR 21-FEB-2001; 2001US-0270134P.

XX PR 27-MAR-2001; 2001US-0278952P.

XX PA (RAWA/) RAMANATHAN C S.

XX PA (FEDE/) FEDER J N.

XX PA (MINT/) MINTIER G A.

XX PI Ramanathan CS, Feder JN, Mintier GA;

XX DR WPI; 2003-521919/49.

XX DR N-ESDB; ACD91434.

XX PT New nucleic acid molecule encoding a human G-protein coupled receptor (HGPRMY25) is useful for diagnosing, preventing or treating diseases involving the receptor, e.g. inflammation, diabetes, asthma, hypertension or cancer.

XX PS Claim 1; Fig 1A-B; 139pp; English.

XX CC The invention describes an isolated nucleic acid molecule comprising a

26 904 52.6 311 4 AAU24572
27 904 52.6 311 5 ABP95702 Human GPC
28 904 52.6 311 5 AAU95730
29 904 52.6 311 5 AAU85192
30 904 52.6 311 7 ADC86331
31 903 52.6 311 4 ABB44529
32 901.5 52.5 314 5 ABP51572
33 901.5 52.5 329 5 ABG76782
34 901 52.4 328 5 ABG76869
35 889.5 51.8 318 4 AAG72154
36 889.5 51.8 318 4 AAU24566
37 889.5 51.8 318 5 ABP95694
38 889.5 51.8 318 5 AAU95718
39 889.5 51.8 318 5 AAU85186
40 889.5 51.8 318 6 ABO42812
41 889.5 51.8 322 5 ABP51560
42 889.5 51.8 324 4 AAG72501
43 888.5 51.7 322 5 ABP51561
44 887.5 51.7 326 6 ABO19498
45 887.5 51.7 339 4 AAG72618

Aau24572 Human Olf
Abp95702 Human GPC
Aau95730 Human Olf
Aau85192 G-coupled
Adc86331 Human GPC
Abb44529 Human GPC
Abp51572 Human G p
Abg76869 Human G-p
Aag72154 Human Olf
Aau24566 Human Olf
Abp95694 Human GPC
Aau95718 Human Olf
Aau85186 G-coupled
Abo42812 G-protein
Abp51560 Human G p
Aag72501 Human OR-
Abp51561 Human G p
Abo19498 Mouse GPC
Aag72618 Murine OR

CC sequence that is at least 95% identical to a polynucleotide encoding
 CC novel human G-protein coupled receptor HGRPMY25. The nucleic acid
 CC molecule, polypeptide and antibody are useful in diagnosing, preventing,
 CC treating or ameliorating medical conditions where GPCR is directly or
 CC indirectly involved, such as immune or inflammatory diseases (e.g.
 CC arthritis, asthma, AIDS, graft-versus-host disease, psoriasis or systemic
 CC lupus erythematosus), reproductive disorders (e.g. varicocele or
 CC orchitis), neural disorders (e.g. Alzheimer's disease, Parkinson's
 CC disease, depression or schizophrenia), cardiovascular disorders (e.g.
 CC hypertension or acute heart failure), pulmonary disorders, endocrine
 CC disorders (e.g. obesity, diabetes or anorexia), bone disorders (e.g.
 CC osteoporosis), pain or cancer. The polynucleotide may also be used in
 CC chromosome identification, in identifying organisms from minute
 CC biological samples, or as molecular weight markers. This is the amino
 CC acid sequence of a novel human HGRPMY25 G-protein coupled receptor
 XX
 SQ Sequence 329 AA;

Query Match 100.0%; Score 1718; DB 6; Length 329;
 Best Local Similarity 100.0%; Pred. No. 7e-181;
 Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSTLGHNMESPHHTDVPSPVFLGIPGLEQFHLWLSLPVCGLGTTATVGNITILVVVA 60
 DB 1 MSSTLGHNMESPHHTDVPSPVFLGIPGLEQFHLWLSLPVCGLGTTATVGNITILVVVA 60

QY 61 TEPVLHKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFHAFQNM 120
 DB 61 TEPVLHKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFHAFQNM 120

QY 121 ESTVLLAMAFDRYVAICHPLRYATILTDITIIAHGVAAVVRGSLMLPCPFFIGRLNFCQ 180
 DB 121 ESTVLLAMAFDRYVAICHPLRYATILTDITIIAHGVAAVVRGSLMLPCPFFIGRLNFCQ 180

QY 181 SHVILHTYCEHMAVVKLAGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRSS 240
 DB 181 SHVILHTYCEHMAVVKLAGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRSS 240

QY 241 HEARSKALGTCGSHVCVILISYTPALFSFTHRFHGHVPHVHIILLANVYLLPPALNPV 300
 DB 241 HEARSKALGTCGSHVCVILISYTPALFSFTHRFHGHVPHVHIILLANVYLLPPALNPV 300

QY 301 YGVGVTQKIRKRVVRVFGSQGMGIKASE 329
 DB 301 YGVGVTQKIRKRVVRVFGSQGMGIKASE 329

RESULT 2
 AAU24646
 ID AAU24646 standard; protein; 329 AA.
 XX AAU24646;
 AC AAU24646;

DT 18-DEC-2001 (first entry)
 XX Human olfactory receptor AOLF141.

DE Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;
 KW food additive; cosmetic; fragrance; pharmaceutical additive.
 XX Homo sapiens.
 OS
 XX WO200168805-A2.
 PN
 XX 20-SEP-2001.
 PD
 XX 13-MAR-2001; 2001WO-US007771.
 PF
 XX 13-MAR-2000; 2000US-0188914P.
 PR
 XX 24-MAR-2000; 2000US-0192033P.
 PR
 XX 12-APR-2000; 2000US-0198474P.
 PR
 XX 24-APR-2000; 2000US-0199335P.
 PR
 XX 26-MAY-2000; 2000US-0207702P.

PR 23-JUN-2000; 2000US-0213849P.
 PR 16-AUG-2000; 2000US-0226534P.
 PR 07-SEP-2000; 2000US-0230732P.
 PR 07-FEB-2001; 2001US-0266862P.
 XX (SENO-) SENOMYX INC.
 PA
 XX Zozulya S;
 PI
 XX WPI; 2001-570867/64.
 DR N-PSDB; AAS42339.
 DR
 XX Nucleic acids encoding human olfactory G protein-coupled receptors,
 PT useful for screening for compounds involved in olfactory sensation, where
 PT the compounds can be used in the food, pharmaceutical and cosmetic
 PT industries to customize odors.
 XX
 XX Claim 60; Page 142; 319pp; English.
 PS
 XX The invention relates to nucleic acids encoding human olfactory
 CC receptors, OR, (a G-protein-coupled receptor, GPCR). The OR's
 CC specifically recognise molecules, odourants, that elicit specific
 CC olfactory sensation. The human olfactory receptors and polynucleotides
 CC encoding them are useful for screening a library of chemical compounds
 CC for compounds that are involved in olfactory sensation. Modulators of
 CC their activity are useful for pharmacological and genetic modulation of
 CC olfactory signalling pathways. Therefore, they can be used in the food,
 CC pharmaceutical and cosmetic industries to customise odours and
 CC fragrances. The present sequence is a human olfactory receptor of the
 CC invention
 XX
 SQ Sequence 329 AA;

Query Match 98.4%; Score 1691; DB 4; Length 329;
 Best Local Similarity 98.8%; Pred. No. 6.7e-178;
 Matches 325; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSSTLGHNMESPHHTDVPSPVFLGIPGLEQFHLWLSLPVCGLGTTATVGNITILVVVA 60
 DB 1 MSSTLGHNMESPHHTDVPSPVFLGIPGLEQFHLWLSLPVCGLGTTATVGNITILVVVA 60

QY 61 TEPVLHKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFHAFQNM 120
 DB 61 TEPVLHKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFHAFQNM 120

QY 121 ESTVLLAMAFDRYVAICHPLRYATILTDITIIAHGVAAVVRGSLMLPCPFFIGRLNFCQ 180
 DB 121 ESTVLLAMAFDRYVAICHPLRYATILTDITIIAHGVAAVVRGSLMLPCPFFIGRLNFCQ 180

QY 181 SHVILHTYCEHMAVVKLAGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRSS 240
 DB 181 SHVILHTYCEHMAVVKLAGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRSS 240

QY 241 HEARSKALGTCGSHVCVILISYTPALFSFTHRFHGHVPHVHIILLANVYLLPPALNPV 300
 DB 241 HEARSKALGTCGSHVCVILISYTPALFSFTHRFHGHVPHVHIILLANVYLLPPALNPV 300

QY 301 YGVGVTQKIRKRVVRVFGSQGMGIKASE 329
 DB 301 YGVGVTQKIRKRVVRVFGSQGMGIKASE 329

RESULT 3
 ABP51578
 ID ABP51578 standard; protein; 329 AA.
 XX ABP51578;
 AC ABP51578;
 XX
 DT 23-SEP-2002 (first entry)
 XX Human G protein coupled receptor SEQ ID NO:38.
 DE Human; G protein coupled receptor; GPCR; GPCRX; neuroprotective;
 KW

KW neotropic; anti-HIV; antiasthmatic; antiarteriosclerotic; cytostatic;
 KW immunomodulator; antiinflammatory; antidiabetic; anorectic; haemostatic;
 KW antibacterial; fungicide; protozoal; virucide; nephrotropic; osteopathic;
 KW cardiant; antiulcer; antiallergic; hepatotropic; antiparkinsonian; HIV;
 KW vaccine; gene therapy; cell signal processing; cardiomyopathy; diabetes;
 KW metabolic pathway modulation; atherosclerosis; cancer; obesity; asthma;
 KW infection; Parkinson's disease; osteoporosis; Crohn's disease; ulcer;
 KW allergy; cirrhosis; glomerulonephritis; stroke; haematopoietic disorder;
 KW systemic lupus erythematosus.
 XX Homo sapiens.
 XX WO200250276-A2.
 XX 27-JUN-2002.
 XX 18-DEC-2001; 2001WO-US049347.
 XX 18-DEC-2000; 2000US-0256635P.
 XX 21-DEC-2000; 2000US-0257876P.
 XX 04-JAN-2001; 2001US-0259743P.
 XX 10-JAN-2001; 2001US-0260718P.
 XX 12-JAN-2001; 2001US-0261498P.
 XX 24-JAN-2001; 2001US-0263689P.
 XX 08-FEB-2001; 2001US-0267464P.
 XX 22-FEB-2001; 2001US-0271021P.
 XX 14-MAR-2001; 2001US-0275946P.
 XX 23-MAR-2001; 2001US-0278150P.
 XX 18-APR-2001; 2001US-0284591P.
 XX 23-APR-2001; 2001US-0285718P.
 XX 19-JUN-2001; 2001US-0299327P.
 XX 16-AUG-2001; 2001US-0312902P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX Li L, Padigaru M, Ballinger RA, Kekuda R, Colman SD, Sciore P,
 PI Smithson G, Peyman JA, Macdougall JR, Stone D, Vernet CAM, Shenoy S;
 PI Gunther E, Millet I, Tchernev VT, Anderson D, Gusev V, Malyankar UM;
 PI Zhong H, Ellerman KE, Wolenc A;
 XX WPI; 2002-557660/59.
 DR N-PSDB; ABQ88372.
 XX
 XX New isolated human G-protein coupled receptor X (GPCRX) polypeptide,
 PT useful for treating or preventing GPCR-associated disorders e.g.
 PT diabetes, atherosclerosis, cancer or obesity.
 XX
 XX Claim 1; Page 88; 354pp; English.
 XX
 CC ABQ88354 to ABQ88417 represent human G protein coupled receptor (GPCR)
 CC cDNA sequences, and ABP51560 to ABP51624 represent human GPCR proteins
 CC from the present invention. GPCR sequences can have neuroprotective,
 CC neotropic, anti-HIV, antiasthmatic, antiarteriosclerotic, cytostatic,
 CC immunomodulator, antiinflammatory, antidiabetic, anorectic, haemostatic,
 CC antibacterial, fungicide, protozoal, virucide, nephrotropic, osteopathic,
 CC cardiant, antiulcer, antiallergic, hepatotropic and antiparkinsonian
 CC activities, and can be used in vaccines and gene therapy. GPCR proteins,
 CC nucleic acid molecules, and antibodies from the present invention can be
 CC used for manufacturing a medicament for treating or preventing a GPCR-
 CC associated disorder or syndrome related to cell signal processing and
 CC metabolic pathway modulation, such as cardiomyopathy, atherosclerosis,
 CC diabetes, cancer, obesity, infections (bacterial, fungal, protozoal or
 CC viral), HIV, asthma, Parkinson's disease, osteoporosis, Crohn's disease,
 CC ulcers, allergies, cirrhosis, glomerulonephritis, stroke, systemic lupus
 CC erythematosus, or haematopoietic disorders. Anti-GPCR antibodies can be
 CC used diagnostically to monitor protein levels in tissues as part of a
 CC clinical testing procedure such as in determining the efficacy of a given
 CC treatment regimen. ABQ88418 to ABQ88639 represent PCR primers and probes
 CC for the human GPCRs of the present invention
 XX
 SQ Sequence 329 AA;

Query Match 98.4%; Score 1691; DB 5; Length 329;

Best Local Similarity 98.8%; Pred. No. 6.7e-178;
 Matches 325; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 MSSTLGHNMESPHRTDVPVFFLLGIPGLEQFHLWLSLPCVGLGTATVGNITILVVVA 60
 Db 1 MSSTLGHNMESPHRTDVPVFFLLGIPGLEQFHLWLSLPCVGLGTATVGNITILVVVA 60
 Qy 61 TEPVLHKPVVFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHFFHAFQMM 120
 Db 61 TEPVLHKPVVFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHFFHAFQMM 120
 Qy 121 ESTVLLAMAFDRYVAICHPLRYATILDTTIIAHGVAAVRGSLMLPCPPFFIGRLNFCQ 180
 Db 121 ESTVLLAMAFDRYVAICHPLRYATILDTTIIAHGVAAVRGSLMLPCPPFFIGRLNFCQ 180
 Qy 181 SHVILHTYCEHMAVVKLACGDTRENRYVGLTAALLNVIGDLCFICLSYALIAQAVLRSS 240
 Db 181 SHVILHTYCEHMAVVKLACGDTRENRYVGLTAALLNVIGDLCFICLSYALIAQAVLRSS 240
 Qy 241 HEARSKALGTGCGSHVCVILISYTPALFSFFTHRGHHVPHVHILLANVYLLPALNPV 300
 Db 241 HEARSKALGTGCGSHVCVILISYTPALFSFFTHRGHHVPHVHILLANVYLLPALNPV 300
 Qy 301 VYGVTKQIRKRVVRVVFQSGQGMGIKASE 329
 Db 301 VYGVTKQIRKRVVRVVFQSGQGMGIKASE 329
 RESULT 4
 ABP51577
 ID ABP51577 standard; protein; 329 AA.
 XX AC ABP51577;
 XX DT 23-SEP-2002 (first entry)
 XX DE Human G protein coupled receptor SEQ ID NO:36.
 XX KW Human; G protein coupled receptor; GPCR; GPCRX; neuroprotective;
 KW neotropic; anti-HIV; antiasthmatic; antiarteriosclerotic; cytostatic;
 KW immunomodulator; antiinflammatory; antidiabetic; anorectic; haemostatic;
 KW antibacterial; fungicide; protozoal; virucide; nephrotropic; osteopathic;
 KW cardiant; antiulcer; antiallergic; hepatotropic; antiparkinsonian; HIV;
 KW vaccine; gene therapy; cell signal processing; cardiomyopathy; diabetes;
 KW metabolic pathway modulation; atherosclerosis; cancer; obesity; asthma;
 KW infection; Parkinson's disease; osteoporosis; Crohn's disease; ulcer;
 KW allergy; cirrhosis; glomerulonephritis; stroke; haematopoietic disorder;
 KW systemic lupus erythematosus.
 XX Homo sapiens.
 OS WO200250276-A2.
 XX 27-JUN-2002.
 XX 18-DEC-2001; 2001WO-US049347.
 XX 18-DEC-2000; 2000US-0256635P.
 XX 21-DEC-2000; 2000US-0257876P.
 XX 04-JAN-2001; 2001US-0259743P.
 XX 10-JAN-2001; 2001US-0260718P.
 XX 12-JAN-2001; 2001US-0261498P.
 XX 24-JAN-2001; 2001US-0263689P.
 XX 08-FEB-2001; 2001US-0267464P.
 XX 14-MAR-2001; 2001US-0271021P.
 XX 23-MAR-2001; 2001US-0275946P.
 XX 18-APR-2001; 2001US-0284591P.
 XX 23-APR-2001; 2001US-0285718P.
 XX 19-JUN-2001; 2001US-0299327P.
 XX 16-AUG-2001; 2001US-0312902P.
 XX
 PA (CURA-) CURAGEN CORP.

XX Li L, Padigaru M, Ballinger RA, Kekuda R, Colman SD, Sciore P;
PI Smithson G, Peyman JA, Macdougall JR, Stone D, Vernet CAM, Shenoy S;
PI Gunther E, Millet I, Tchernev VT, Anderson D, Gusev V, Malyankar UM;
PI Zhong H, Ellerman KE, Wolenc A;
DR WPI; 2002-557660/59.
DR N-PSDB; ABQ88371.
XX
XX New isolated human G-protein coupled receptor X (GPCRX) polypeptide,
PT useful for treating or preventing GPCR-associated disorders e.g.
PT diabetes, atherosclerosis, cancer or obesity.
XX
XX Claim 1; Page 88; 354pp; English.
XX
XX ABQ88354 to ABQ88417 represent human G protein coupled receptor (GPCR)
CC cDNA sequences, and ABP51560 to ABP51624 represent human GPCR proteins
CC from the present invention. GPCR sequences can have neuroprotective,
CC nootropic, anti-HIV, antiasthmatic, antiarteriosclerotic, cyostatic,
CC immunomodulator, antiinflammatory, antidiabetic, anorectic, haemostatic,
CC antibacterial, fungicide, protozoal, virucide, nephrotropic, osteopathic,
CC cardiant, antiulcer, antiallergic, hepatotropic and antiparkinsonian
CC activities, and can be used in vaccines and gene therapy. GPCR proteins,
CC nucleic acid molecules, and antibodies from the present invention can be
CC used for manufacturing a medicament for treating or preventing a GPCR-
CC associated disorder or syndrome related to cell signal processing and
CC metabolic pathway modulation, such as cardiomyopathy, atherosclerosis,
CC diabetes, cancer, obesity, infections (bacterial, fungal, protozoal or
CC viral), HIV, asthma, Parkinson's disease, osteoporosis, Crohn's disease,
CC ulcers, allergies, cirrhosis, glomerulonephritis, stroke, systemic lupus
CC erythematosus, or haematopoietic disorders. Anti-GPCR antibodies can be
CC used diagnostically to monitor protein levels in tissues as part of a
CC clinical testing procedure such as in determining the efficacy of a given
CC treatment regimen. ABQ88418 to ABQ88639 represent PCR primers and probes
CC for the human GPCRs of the present invention
XX
XX Sequence 329 AA;
XX
XX Query Match 98.4%; Score 1691; DB 5; Length 329;
XX Best Local Similarity 98.8%; Pred. No. 6.7e-178;
XX Matches 325; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 MSSTLGHNMESPHHTDVPDPSVFFLLGIPGLQFHLWLSLPVCGLTATVGNITILVVVA 60
XX Db 1 MSSTLGHNMESPHHTDVPDPSVFFLLGIPGLQFHLWLSLPVCGLTATVGNITILVVVA 60
XX
XX QY 61 TEPVLHKPYYLFLCMLSTIDLAASVSTVPKLLAIFWCAGHISASACLAHFFIHAFCWM 120
XX Db 61 TEPVLHKPYYLFLCMLSTIDLAASVSTVPKLLAIFWCAGHISASACLAHFFIHAFCWM 120
XX
XX QY 121 ESTVLLAMAFDRYVAICHPLRYATILTDITIAHIGVAAVVRGSLMLPCPFIFGLNFCQ 180
XX Db 121 ESTVLLAMAFDRYVAICHPLRYATILTDITIAHIGVAAVVRGSLMLPCPFIFGLNFCQ 180
XX
XX QY 181 SHVILHTYCEHMAVVKLACGTRPNRVYGLTAALLIVGDLFCIGLSYALIAQAVLRSS 240
XX Db 181 SHVILHTYCEHMAVVKLACGTRPNRVYGLTAALLIVGDLFCIGLSYALIAQAVLRSS 240
XX
XX QY 241 HEARSKALGTGSHVCVILISYTPALFSFFTHRRFGHHVPVHIHILLANVYLLPPALNPV 300
XX Db 241 HEARSKALGTGSHVCVILISYTPALFSFFTHRRFGHHVPVHIHILLANVYLLPPALNPV 300
XX
XX QY 301 VYGKTKQIRKRVVRVFGSGQGMGIKASE 329
XX Db 301 VYGKTKQIRKRVVRVFGSGQGMGIKASE 329
XX
XX RESULT 5
XX ID ABP95772
XX AC ABP95772 standard; protein; 329 AA.
XX AC ABP95772;
XX

DT 06-MAR-2003 (first entry)
XX Human GPCR polypeptide SEQ ID NO 354.
XX Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
XX drug development; gustatory; taste; fragrance; receptor.
XX Homo sapiens.
XX WO200216548-A2.
XX 28-FEB-2002.
XX 30-JUL-2001; 2001WO-IB001446.
XX 04-AUG-2000; 2000JP-00237818.
XX 13-FEB-2001; 2001JP-00034434.
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX Haga T, Takeda S, Mitaku S;
XX WPI; 2002-304118/34.
XX N-PSDB; ABZ43046.
XX Database global search for G protein-coupled receptors, proteins and
XX encoded genes for studying in vivo signal transduction mechanism and
XX identifying targets for drug development.
XX Claim 10; SEQ ID NO 354; 97pp + Sequence Listing; Japanese.
XX The invention relates to a method for screening G protein-coupled
XX receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-
XX ABP95942) by extracting open-reading frames containing 6-8 transmembrane
XX domains with 250-1000 amino acid residues to give a gene homologous with
XX a known GPCR gene. The receptor proteins and encoded genes are useful for
XX studying in vivo signal transduction mechanism and identifying targets
XX for drug development e.g. based on olfactory and gustatory receptors in
XX form of agonists and antagonists by screening intrinsic and extrinsic
XX ligands as bitter taste inhibitors, taste enhancers and fragrance
XX improvers. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 329 AA;
XX
XX Query Match 98.4%; Score 1691; DB 5; Length 329;
XX Best Local Similarity 98.8%; Pred. No. 6.7e-178;
XX Matches 325; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 MSSTLGHNMESPHHTDVPDPSVFFLLGIPGLQFHLWLSLPVCGLTATVGNITILVVVA 60
XX Db 1 MSSTLGHNMESPHHTDVPDPSVFFLLGIPGLQFHLWLSLPVCGLTATVGNITILVVVA 60
XX
XX QY 61 TEPVLHKPYYLFLCMLSTIDLAASVSTVPKLLAIFWCAGHISASACLAHFFIHAFCWM 120
XX Db 61 TEPVLHKPYYLFLCMLSTIDLAASVSTVPKLLAIFWCAGHISASACLAHFFIHAFCWM 120
XX
XX QY 121 ESTVLLAMAFDRYVAICHPLRYATILTDITIAHIGVAAVVRGSLMLPCPFIFGLNFCQ 180
XX Db 121 ESTVLLAMAFDRYVAICHPLRYATILTDITIAHIGVAAVVRGSLMLPCPFIFGLNFCQ 180
XX
XX QY 181 SHVILHTYCEHMAVVKLACGTRPNRVYGLTAALLIVGDLFCIGLSYALIAQAVLRSS 240
XX Db 181 SHVILHTYCEHMAVVKLACGTRPNRVYGLTAALLIVGDLFCIGLSYALIAQAVLRSS 240
XX
XX QY 241 HEARSKALGTGSHVCVILISYTPALFSFFTHRRFGHHVPVHIHILLANVYLLPPALNPV 300
XX Db 241 HEARSKALGTGSHVCVILISYTPALFSFFTHRRFGHHVPVHIHILLANVYLLPPALNPV 300
XX
XX QY 301 VYGKTKQIRKRVVRVFGSGQGMGIKASE 329
XX Db 301 VYGKTKQIRKRVVRVFGSGQGMGIKASE 329
XX

RESULT 6	
AAU85266	
AAU85266 standard; protein; 329 AA.	
XX	
XX	
AAU85266;	
XX	
08-MAY-2002 (first entry)	
XX	
G-coupled olfactory receptor #127.	
XX	
Human; olfactory G-coupled receptor; sensory perception of odourant;	
KW odour composition; taste composition.	
XX	
Homo sapiens.	
OS	
WO200198526-A2.	
XX	
27-DEC-2001.	
XX	
22-JUN-2001; 2001WO-US020122.	
XX	
22-JUN-2000; 2000US-0213812P.	
PR	
13-MAR-2001; 2001US-00804291.	
XX	
(SENSO-) SENOMYX INC.	
PA	
Zozulya S, Stryer L;	
PI	
XX	
WPI; 2002-083330/11.	
DR	
N-PSDB; ABK37625.	
XX	
Representing sensory perception of one or more odorants for the	
PT identification and design of tastes and odors comprises providing a	
PT representative group of n olfactory receptors.	
XX	
Claim 1; Page 115; 182pp; English.	
XX	
The invention relates to a method of representing sensory perception of	
CC one or more odorants. The method comprises: (a) providing a	
CC representative class of n olfactory receptors or ligand binding domains	
CC (LBD) of these receptors; (b) measuring values X1 to Xn representative of	
CC at least one activity of one or more odorants selected from: (i) binding	
CC one or more odorants to the LBD of at least one of the n olfactory	
CC receptors; (ii) activating at least one of the n olfactory receptors with	
CC the one or more odorants; and (iii) blocking at least one of the n	
CC olfactory receptors with the one or more odorants; and (c) generating a	
CC representation of sensory perception from the values X1 to Xn. The	
CC representation of the sensory perception of odorants is useful for the	
CC design and formulation of odour and taste compositions. AAU85140-AAU85393	
CC represent human olfactory G-coupled receptor amino acid sequences of the	
XX invention	
XX	
Sequence 329 AA;	
Query Match	98.4%; Score 1591; DB 5; Length 329;
Best Local Similarity	98.8%; Pred. No. 6.7e-178;
Matches 325; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	
Qy	1 MSSTLGHNMESPHHTDVPVSFFLLIGICGLEQFHLWLSLPVCGLGCTATVGNITILVVA 60
Db	1 MSSTLGHNMESPHNTDVPVSFFLLIGICGLEQFHLWLSLPVCGLGCTATVGNITILVVA 60
Qy	61 TEPVLHKPVYFLCMLSTIDLAAASVSTVPKLLAIFWCAGAGHISASACLAHMFHIFACMM 120
Db	61 TEPVLHKPVYFLCMLSTIDLAAASVSTVPKLLAIFWCAGAGHISASACLAQMFFHIFACMM 120
Qy	121 ESTVLLNAFAORYVAICHPLRYATILTTDIIAHIGVAAVVRGSLMLPCPFPIGRINFCQ 180
Db	121 ESTVLLNAFAORYVAICHPLRYATILTTDIIAHIGVAAVVRGSLMLPCPFPIGRINFCQ 180
Qy	181 SHVILHTYCEHMAVVKIACGDRPNRNVYGLTAAALLVIGVDLFCIGLSYALIAQAVLRSS 240

Db 121 ESTVLLAMAFDRYAICHPLRYATILTDITIAHIGVAAVVRGSLMLPCPFLIGRLNFQ 180
 QY 181 SHVILHTYCEHMAVVKACGDRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRSS 240
 Db 181 SHVILHTYCEHMAVVKACGDRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRSS 240
 QY 241 HEARSKALGTCGSHVCVILISYTPALFSFTHRGHHVPVHIHILLANVYLLPPALNPV 300
 Db 241 HEARSKALGTCGSHVCVILISYTPALFSFTHRGHHVPVHIHILLANVYLLPPALNPV 300
 QY 301 VYGVTKQIRKRVVRVFSQGGMGKASE 329
 Db 301 VYGVTKQIRKRVVRVFSQGGMGKASE 329

RESULT 8

AAG71674
 ID AAG71674 standard; protein; 321 AA.

XX AAG71674;

DT 30-JUL-2001 (first entry)

DE Human olfactory receptor polypeptide, SEQ ID NO: 1355.

KW Human; olfactory receptor; OR; primary scent determination;

KW secondary scent determination; polypeptide library; odour receptor;

XX scent profile; scent fingerprint; scent representation.

OS Homo sapiens.

PN WO200127158-A2.

PD 19-APR-2001.

PF 06-OCT-2000; 2000WO-US027582.

XX 08-OCT-1999; 99US-0158615P.

PR 24-FEB-2000; 2000US-0184809P.

XX (DIGI-) DIGISCENTS.

PA (YEDA) YEDA RES & DEV CO LTD.

XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

DR WPI; 2001-290713/30.

XX New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists.

PS Claim 11; Page 838-839; 1857pp; English.

CC The present sequence is an olfactory receptor which is encoded by one of
 CC a number of novel polynucleotides. The polynucleotides can be used in
 CC screening for olfactory agonists and antagonists. The methods allow for
 CC the determination of primary scents and the identification of the odour
 CC receptors used to detect these primary scents. The methods also enable
 CC determination of secondary scents and the identification of combinations
 CC of odour receptors that are involved in detecting such secondary scents.
 CC This enables the construction of a scent representation (also called a
 CC scent fingerprint or scent profile), which may be used to re-create and
 CC edit scents. Libraries of olfactory receptors are useful for determining
 CC the interaction pattern of a composition with the receptors, and can be
 CC used for determining differences in the olfactory faculties of different
 CC individuals

XX Sequence 321 AA;

Query Match

Best Local Similarity 96.0%; Score 1649; DB 4; Length 321;

Matches 317; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 MESPHTDVPDFVLLGIPGLEQFHLWLSLPVCGLTATVGNITILVVATEPVLHKP 68

Db 1 MESPHTDVPDFVLLGIPGLEQFHLWLSLPVCGLTATVGNITILVVATEPVLHKP 60
 QY 69 VYLFCLMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAHMFHAFCMMESTVLLAM 128
 Db 61 VYLFCLMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAQWFFHAFCMMESTVLLAM 120
 QY 129 AFDYVAICHPLRYATILTDITIAHIGVAAVVRGSLMLPCPFFIGRLNFQSHVILHTY 188
 Db 121 AFDYVAICHPLRYATILTDITIAHIGVAAVVRGSLMLPCPFFIGRLNFQSHVILHTY 180
 QY 189 CEHMAVVKACGDRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRSSSHEARSKAL 248
 Db 181 CEHMAVVKACGDRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVLRSSSHEARSKAL 240
 QY 249 GTCGSHVCVILISYTPALFSFTHRGHHVPVHIHILLANVYLLPPALNPVYGVTKQ 308
 Db 241 GTCGSHVCVILISYTPALFSFTHRGHHVPVHIHILLANVYLLPPALNPVYGVTKQ 300
 QY 309 IRKRVVRVFSQGGMGKASE 329
 Db 301 IRKRVVRVFSQGGMGKASE 321

RESULT 9

AAU80511

ID AAU80511 standard; protein; 321 AA.

XX AAU80511;

DT 12-MAR-2002 (first entry)

DE Human G-coupled receptor (GCREC) protein, Seq ID No 19.

KW Human; cytostatic; neuroprotective; immunosuppressant; nootropic;
 KW anti-inflammatory; anti-viral; gastrointestinal; cardiovascular;
 KW cerebroprotective; G-coupled receptor; cell proliferative disease;
 KW lymphoma; leukaemia; breast cancer; cirrhosis; neurological disorder;
 KW stroke; Alzheimer's disease; multiple sclerosis; mental retardation;
 KW cardiovascular disease; atherosclerosis; angina pectoris; indigestion;
 KW congestive heart failure; gastrointestinal disorder; dysphagia; AIDS;
 KW gastritis; autoimmune disorder; inflammatory disorder; Crohn's disease;
 KW systemic lupus erythematosus; metabolic disorder; diabetes; obesity;
 KW viral infection; herpesvirus; parvovirus;
 KW acquired immune deficiency syndrome.

OS Homo sapiens.

PN WO200190359-A2.

PD 29-NOV-2001.

XX 22-MAY-2001; 2001WO-US016833.

XX 22-MAY-2000; 2000US-0206222P.

PR 25-MAY-2000; 2000US-0207476P.

PR 02-JUN-2000; 2000US-0208834P.

PR 02-JUN-2000; 2000US-0208861P.

PR 07-JUN-2000; 2000US-0209868P.

XX (INCY-) INCYTE GENOMICS INC.

XX Patterson C, Tribouley CM, Yao MG, Griffin JA, Thornton M, Lu Y;

PI Kallick DA, Gandhi AR, Au-Young J;

XX WPI; 2002-106199/14.

DR N-PSDB; ABK16633.

XX New G-protein coupled receptors useful for treating or preventing cell
 PT proliferative (e.g. leukemia), neurological (e.g. stroke), cardiovascular
 PT or autoimmune/inflammatory disorders.

PS Claim 1; Page 133-134; 149pp; English.

XX CC The invention relates to a novel human G-coupled receptor (I). (I) and
 CC its corresponding polynucleotides are useful for diagnosing, treating or
 CC preventing cell proliferative diseases (e.g. lymphoma, leukaemia, breast
 CC cancer or chondrosarcoma), neurological disorders (e.g. stroke, Alzheimer's
 CC disease, multiple sclerosis or mental retardation), cardiovascular
 CC diseases (e.g. atherosclerosis, angina pectoris or congestive heart
 CC failure), gastrointestinal disorders (e.g. dysphagia, indigestion or
 CC gastritis), autoimmune/inflammatory disorders (e.g. AIDS, Crohn's disease
 CC or systemic lupus erythematosus) or metabolic disorders (e.g. diabetes or
 CC obesity), or viral infections (e.g. infection by herpesvirus or
 CC parvovirus). AAU80493-AAU80515 represent novel human G-coupled receptor
 CC amino acid sequences of the invention
 XX Sequence 321 AA;
 CC
 CC Query Match 96.0%; Score 1649; DB 5; Length 321;
 CC Best Local Similarity 98.8%; Pred. No. 2.8e-173;
 CC Matches 317; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 9 MESPHHTDVDSVFFLLGIPGLEQPHLWLSLPVCGLTATVGNITILVVVATEPVLHKP 68
 Db 1 MESPNHTDVDSVFFLLGIPGLEQPHLWLSLPVCGLTATVGNITILVVVATEPVLHKP 60
 QY 69 VYFLCMLSTIDLAASVSTVPKLLAI FWCAGHISASACLAHMFTHAFCMESTVLLAM 128
 Db 61 VYFLCMLSTIDLAASVSTVPKLLAI FWCAGHISASACLAHMFTHAFCMESTVLLAM 120
 QY 129 AFDRYVAICHPLRYATILTDITIIAHIGVAAVVRGSLMLPCPFFIGRLNFCQSHVILHTY 188
 Db 121 AFDRYVAICHPLRYATILTDITIIAHIGVAAVVRGSLMLPCPFFIGRLNFCQSHVILHTY 180
 QY 189 CEHMAVVKACGDTPRNRYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSHEARSKAL 248
 Db 181 CEHMAVVKACGDTPRNRYGLTAALLVIGVDLFCIGLSYALSAQAVLRLSHEARSKAL 240
 QY 249 GTCGSHVCVILLISYTPALFSFTHRHGHVPHIHLANVYLLPPALNPVYGVKTKQ 308
 Db 241 GTCGSHVCVILLISYTPALFSFTHRHGHVPHIHLANVYLLPPALNPVYGVKTKQ 300
 QY 309 IRKRVVRVFSQGGMGKIKASE 329
 Db 301 IRKRVVRVFSQGGMGKIKASE 321
 RESULT 10
 AAU95725
 ID AAU95725 standard; protein; 321 AA.
 AC AAU95725;
 XX AAU95725;
 XX 02-JUL-2002 (first entry)
 DE Human olfactory and pheromone G protein-coupled receptor #212.
 KW Human; olfactory and pheromone G protein coupled; receptor; GPCR;
 KW tranquilizer; antidepressant; neuroleptic; endocrine; anabolic;
 KW anorectic; taste; fragrance; food additive; cosmetic; cell migration;
 KW sterility; psychotic disorder; neurological disorder; anxiety;
 KW schizophrenia; manic depression; depression; axonal growth;
 KW menstrual cycle; appetite sexual motivation; sexual attraction;
 KW aggression.
 XX Homo sapiens.
 OS
 XX WO200224726-A2.
 PN
 XX 28-MAR-2002.
 PD
 XX 21-SEP-2001; 2001WO-BE000162.
 PF
 XX 22-SEP-2000; 2000EP-00870211.
 PR
 XX

(CHEM-) CHEMCOM SA.
 Veithen A;
 WPI; 2002-330013/36.
 N-PSDB; ABK68612.
 Novel pheromone G-protein coupled receptor and receptor-derived agonists,
 antagonists or inhibitors useful in food or cosmetic products or in the
 treatment or prevention of neurological disorders such as anxiety and
 schizophrenia.
 Disclosure; Page 647-648; 833pp; English.
 The invention relates to olfactory and pheromone G-protein coupled
 receptor (GPCR) or a protein 95% identical to the GPCR, a specific active
 portion and its encoding polynucleotide. Also included are an agonist,
 antagonist or inhibitor of the GPCR or the polynucleotide, a vector
 comprising the polynucleotide, a cell transformed by the vector, a non-
 human mammal comprising a partial or total deletion of the polynucleotide
 encoding the receptor and screening (detection and possibly, recovering)
 of compounds which are known or not known to be agonist, antagonists or
 inhibitors of natural compounds to the GPCR. The receptor-derived
 agonists, antagonists, inhibitors or compounds are used as an
 improvement, elimination or substitution of an existing taste and/or a
 fragrance of (or in) the food and/or cosmetic products. They can also be
 used in the preparation of medicament in the treatment and/or prevention
 of a mammalian disorder, such as cell migration, sterility, psychotic and
 neurological disorders, including anxiety, schizophrenia, manic
 depression, depression, for promoting axonal growth, nerve cell
 connection and nerve regeneration for modulating male and female
 endocrine functions, hormone production and the menstrual cycle, for the
 prevention or the treatment by stimulation of several mammalian
 behaviours, such as stimulation or suppression of appetite, sexual
 motivation, sexual attraction, aggression and for promoting or
 suppressing chemical communication between organisms. The present
 sequence is a human olfactory and pheromone GPCR protein sequence
 XX Sequence 321 AA;
 QY 9 MESPHHTDVDSVFFLLGIPGLEQPHLWLSLPVCGLTATVGNITILVVVATEPVLHKP 68
 Db 1 MESPNHTDVDSVFFLLGIPGLEQPHLWLSLPVCGLTATVGNITILVVVATEPVLHKP 60
 QY 69 VYFLCMLSTIDLAASVSTVPKLLAI FWCAGHISASACLAHMFTHAFCMESTVLLAM 128
 Db 61 VYFLCMLSTIDLAASVSTVPKLLAI FWCAGHISASACLAHMFTHAFCMESTVLLAM 120
 QY 129 AFDRYVAICHPLRYATILTDITIIAHIGVAAVVRGSLMLPCPFFIGRLNFCQSHVILHTY 188
 Db 121 AFDRYVAICHPLRYATILTDITIIAHIGVAAVVRGSLMLPCPFFIGRLNFCQSHVILHTY 180
 QY 189 CEHMAVVKACGDTPRNRYGLTAALLVIGVDLFCIGLSYALIAQAVLRLSHEARSKAL 248
 Db 181 CEHMAVVKACGDTPRNRYGLTAALLVIGVDLFCIGLSYALSAQAVLRLSHEARSKAL 240
 QY 249 GTCGSHVCVILLISYTPALFSFTHRHGHVPHIHLANVYLLPPALNPVYGVKTKQ 308
 Db 241 GTCGSHVCVILLISYTPALFSFTHRHGHVPHIHLANVYLLPPALNPVYGVKTKQ 300
 QY 309 IRKRVVRVFSQGGMGKIKASE 329
 Db 301 IRKRVVRVFSQGGMGKIKASE 321
 RESULT 11
 ABR01673
 ID ABR01673 standard; protein; 316 AA.
 XX

QY 189 CEHMAVVKLACDTRPNRVYGLTAALLIVGVDFLCIGLSYALIAQAVLRLSHSKAL 248
 DB 180 CEHMAVVKLACGGTQPNNIYGITATLVVGTDSICIAVSALIDRAVLGLSKKARAKTF 239
 QY 249 GTCGSHVCVILISYPALFSTFTHRFHGHVPHIHLILLANVVLPPALNPVYGVKTKQ 308
 DB 240 GTCGSHLGVILLFYTFLGFSYTFQRFQGVPRHIHLADLYLVVPPMLNPIIYGMKTKQ 299
 QY 309 IRKRVVRVFSQ 320
 DB 300 IWDGALRLKKG 311
 RESULT 13
 ID ABR01670 standard; protein; 316 AA.
 AC ABR01670;
 DT 17-APR-2003 (first entry)
 DE Human G protein coupled receptor SEQ ID 200.
 KW Human; anorectic; antiasthmatic; antidiabetic; hypotensive; receptor;
 KW antiparkinsonian; nootropic; neuroprotective; tranquiliser;
 KW antirheumatic; antiinflammatory; osteopathic; cardiant; neuroleptic;
 KW antiarthritic; gene therapy; olfactory G protein-coupled receptor; GPCR;
 KW infection; obesity; diabetes; hypertension; malnutrition;
 KW Parkinson's disease; Alzheimer's disease; Korsakoff's psychosis; anxiety;
 KW rheumatoid arthritis; chronic obstructive pulmonary disease;
 KW osteoporosis; asthma; myocardial infarction; schizophrenia;
 KW osteoarthritis.
 OS Homo sapiens.
 XX WO2003000735-A2.
 PN 03-JAN-2003.
 PD 24-JUN-2002; 2002WO-IB002481.
 PF 26-JUN-2001; 2001US-0301095P.
 PR 06-NOV-2001; 2001US-0332758P.
 XX (DECO-) DECODE GENETICS EHF.
 PA Martinez RAM, Sigurdsson GT;
 PI WPI; 2003-175284/17.
 DR N-PSDB; ABZ77971.
 XX New olfactory G protein-coupled receptor gene nucleic acid and
 PT polypeptide, useful for diagnosing or treating a disease or condition
 PT associated with GPCR, e.g. obesity, diabetes, hypertension, malnutrition
 PT or Alzheimer's disease.
 XX Claim 9; Page 100-101; 383pp; English.
 PS The present invention relates to novel human olfactory G protein-coupled
 CC receptors (GPCR) and their coding sequences (ABZ77872-ABZ77986 and
 CC ABR01571-ABR01685). The GPCRs and coding sequences are useful for
 CC diagnosing or treating a disease or condition associated with GPCR, e.g.
 CC infections, obesity, diabetes, hypertension, malnutrition, Parkinson's
 CC disease, Alzheimer's disease, Korsakoff's psychosis, anxiety, rheumatoid
 CC arthritis, chronic obstructive pulmonary disease, osteoporosis, asthma,
 CC myocardial infarction, schizophrenia, or osteoarthritis
 XX Sequence 316 AA;
 SQ Query Match 55.3%; Score 950.5; DB 6; Length 316;
 Best Local Similarity 58.1%; Pred. No. 4.1e-96;
 Matches 175; Conservative 50; Mismatches 75; Indels 1; Gaps 1;

QY 18 DPSVEFLGIPGLBQFHLMSLPVCGGLGTATVGNITLVVVVATEPVLHKPVYFLCMLS 77
 DB 9 NPTSLFLMGIPGEASHFWIAFFPCSMYALAVGMVVLLVHSEPVHLHQPMYFLCMLS 68
 QY 78 TIDLAASVSTVPKLLAIFWCAGAGHISASACLAHMEFFIHAFQWMBESTVILLAMAFDRYVAIC 137
 DB 69 TIDLVTCTSTVPKLLALFWAKDAEINFGACAAQMEFFIHGFSAVESGILLAMAFDRYLAIC 128
 QY 138 HPLRYATILDTTIAHIGVAAVVRGSLMLPCPPFIIGRLNFCQSHVILHTYCEHMAVVKL 197
 DB 129 WPLHYGSLSPESVGLGAAVLRGLGLMTPUTCLLARLSYC-SRVVAHSYCEHMAVVKL 187
 QY 198 ACGDTRPNRVYGLTAALLIVGVDFLCIGLSYALIAQAVLRLSHSKALGTCGSHVCV 257
 DB 188 ACGGTQPNNIYGITATLVVGTDSICIAVSALIDRAVLGLSKKARAKTFGTCGSHLGV 247
 QY 258 ILISYTPALFSTFTHRFHGHVPHIHLILLANVVLPPALNPVYGVKTKQIRKEVVRVF 317
 DB 248 ILLFYTFLGFSYTFQRFQGVPRHIHLADLYLVVPPMLNPIIYGMKTKQIWDGALRLK 307
 QY 318 Q 318
 DB 308 K 308
 RESULT 14
 ADC86381
 ID ADC86381 standard; protein; 299 AA.
 AC ADC86381;
 XX 01-JAN-2004 (first entry)
 DT Human GPCR protein SEQ ID NO:834.
 DE human; GPCR; guanosine triphosphate-binding protein coupled receptor;
 KW gene therapy.
 XX Homo sapiens.
 OS EP1270724-A2.
 PN 02-JAN-2003.
 PD 18-JUN-2002; 2002EP-00013517.
 PF 18-JUN-2001; 2001JP-00246789.
 PR (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 XX Suwa M, Asai K, Akiyama Y, Aburatani H;
 PI WPI; 2003-315783/31.
 DR N-PSDB; ADC86380.
 XX New polynucleotide, useful for preparing a composition for treating a
 PT patient in need of increased or suppressed activity or expression of the
 PT guanosine triphosphate-binding protein coupled receptor.
 XX Claim 2; SEQ ID NO 834; 28pp; English.
 PS The invention relates to a novel polynucleotide encoding a guanosine
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
 CC the invention may have a use in gene therapy. The polynucleotide and
 CC polypeptide are useful for preparing a composition for treating a patient
 CC in need of increased or suppressed activity or expression of the
 CC guanosine triphosphate-binding protein coupled receptor. The protein
 CC sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
 XX Sequence 299 AA;
 SQ Query Match 54.5%; Score 936.5; DB 7; Length 299;

Best Local Similarity 58.4%; Pred. No. 1.3e-94;
Matches 173; Conservative 48; Mismatches 74; Indels 1; Gaps 1;
QY 25 LGIPGLEQHLWLSLPCVGLGTATIGNITILVVVATEPVHLKPVYFLCMLSTIDLAAS 84
Db 1 MGIPGPEASHFWIAFFPCSMYALAVLGNVMVLLVHSEPVHLQHPMYFLCMLSTIDLVLC 60
QY 85 VSTVPKLLAIFWCGAGHISASACLAHMFTHAFCMMESTVLLAMAFDRYVAICHPLRYAT 144
Db 61 TSTVPKLLALFWAKDREINFGACAAQMFHLHGSFSAVESGILLAMAFDRYVAICWPLHYGS 120
QY 145 ILTDTIIAHIGVAAVVRGSLMLPCPFHGRNFCQSHVILHTYCEHMAVVKLACGDTTP 204
Db 121 LLSPEVGKLGAAVLRGLGMLTFLCCLARLSYC-SRVVAHGYCEHMAVVKLACGDTQ 179
QY 205 NRVYGLTAALLVIGVDLFCIGLSYALIAQAVALRSLSSHEARSKALGTCGSHVCLISYTP 264
Db 180 NNIIYGITATLVVGTDSICIAVSAYALIRAVLGLSSKEARAKTFGTGSHLGVILLFYTP 239
QY 265 ALFSFTHRFHGHVPHVHILLANVYLLPPALNPVYGVKTKQIRKRVURVQSG 320
Db 240 GLFSFTQRFQGVPHRHILLADLVVPPMLNPIIYGKTKQIWDGALLDKWG 295

RESULT 15
AAG72396
ID AAG72396 standard; protein; 314 AA.
XX AAG72396;
XX
DT 30-JUL-2001 (first entry)
XX Human OR-like polypeptide query sequence, SEQ ID NO: 2077.
DE Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation.
XX Homo sapiens.
XX
XX WO200127158-A2.
XX
XX 19-APR-2001.
XX
XX 06-OCT-2000; 2000WO-US027582.
XX
XX 08-OCT-1999; 99US-0158615P.
XX 24-FEB-2000; 2000US-0184809P.
XX
XX (DIGI-) DIGISCENTS.
XX (YEDA) YEDA RES & DEV CO LTD.
XX
XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX WPI; 2001-290713/30.
XX

New polynucleotides which encode polypeptides involved in olfactory
sensations for identifying olfactory agonists and antagonists.
Example 6; Page 1393; 1857pp; English.

The present sequence is a polypeptide encoded by one of 344 newly mined
human genes. It was used as a query sequence in a database search of
olfactory receptor (OR)-like sequences. The invention relates to isolated
polynucleotides encoding polypeptides involved in olfactory sensation.
The polynucleotides can be used in screening for olfactory agonists and
antagonists. The methods allow for the determination of primary scents
and the identification of the odour receptors used to detect these
primary scents. The methods also enable determination of secondary scents
and the identification of combinations of odour receptors that are
involved in detecting such secondary scents. This enables the
construction of a scent representation (also called a scent fingerprint
or scent profile), which may be used to re-create and edit scents.

CC Libraries of olfactory receptors are useful for determining the
CC interaction pattern of a composition with the receptors, and can be used
CC for determining differences in the olfactory faculties of different
CC individuals
XX
SQ Sequence 314 AA;

Query Match 54.2%; Score 931.5; DB 4; Length 314;
Best Local Similarity 59.9%; Pred. No. 5.1e-94;
Matches 179; Conservative 42; Mismatches 77; Indels 1; Gaps 1;

QY 19 PSVFELLPGLEQHLWLSLPCVGLGTATIGNITILVVVATEPVHLKPVYFLCMLST 78
Db 13 PS-FLLVGPGLSESHWIALPLGILYLLALVGNVTILFIWMDPSLHOSMYFLSLMLAA 71
QY 79 IDLAASVSTVPKLLAIFWCGAGHISASACLAHMFTHAFCMMESTVLLAMAFDRYVAICH 138
Db 72 IDLVLASSTAPKALAVLLVHAHEIGYIVCLIQMFFTHAFSSMESGLVAMALDRYVAICH 131
QY 139 PLRYATILDTTIIAHIGVAAVVRGSLMLPCPFHGRNFCQSHVILHTYCEHMAVVKLA 198
Db 132 PLHSTILPHPGVIGRIGVMVLRGLLILPFFLITGLTFLFCQATIIIGHAYCEHMAVVKLA 191
QY 199 CGDTRPNRVYGLTAALLVIGVDLFCIGLSYALIAQAVALRSLSSHEARSKALGTCGSHVCVI 258
Db 192 CSETTVNRAYGLTMALLVIGLDVLAIGVSYAHILQAVLKVPGSEARKLAFSTCGSHICVI 251
QY 259 LISYTPALFSFTHRFHGHVPHVHILLANVYLLPPALNPVYGVKTKQIRKRVURVF 317
Db 252 LVFYVPGIFSFTHRFHGHVPHVHILLATRYLLMPPALNPVYGVKTKQIRQVLRVF 310

Search completed: September 15, 2004, 21:36:23
Job time : 60 secs